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Sequence Listing

<110> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan l.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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 cgcgctggac accatgtgga tcttgggtct gaggaagaa tttgaggaag 950
 ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
 aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050
 ccacctgtct ggggacagcc tcttcctgag gaaagctgag gattttggaa 1100
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 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300
 cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
 caataccac agtggcctct tcaccacct gggcgtattc acgctgggcg 1400
 ccagggccga cagctactat gactacctgc tgaagcagt gatccaggcg 1450
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 tgtcagaacg cacctgctgc ggactccga gccagtaag ctcaccttg 1550
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<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

Met	Ala	Ala	Cys	Glu	Gly	Arg	Arg	Ser	Gly	Ala	Leu	Gly	Ser	Ser
1				5					10					15

Gln	Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala
				20					25					30

Val	Ala	Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro
				35					40					45

His	Arg	Asp	Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr
				50					55					60

Asp	Asn	Ser	Lys	Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp
				65					70					75

Lys	Gln	Leu	Ser	Arg	Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu
				80					85					90

Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala
				95					100					105

Asp His Trp Lys	Ala Leu Ala Phe Arg	Leu Glu Glu Glu Gln Lys	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu Lys	Pro Ala Asn Pro Pro Val	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp Thr	Asp Pro Glu Asn Leu Pro	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln Arg	His Ile Gln Arg Gly Pro	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro Ser	Gln Asp Leu Lys Asp Gly	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg Gln	Glu Ala Pro Val Asp Pro	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg Thr	Val Ile Ser Trp Arg Gly	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly Thr	Glu Leu Pro Ser Arg Arg	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro Leu	Pro Pro Ala Arg Thr Gln	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr Arg	Gln Lys Gly Val Ile Asp	245	250	255
Val Phe Leu His	Ala Trp Lys Gly Tyr	Arg Lys Phe Ala Trp Gly	260	265	270
His Asp Glu Leu	Lys Pro Val Ser Arg	Ser Phe Ser Glu Trp Phe	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp Ala	Leu Asp Thr Met Trp Ile	290	295	300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val Ser	305	310	315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe Glu	320	325	330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His Leu	335	340	345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly Asn	350	355	360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr Ser	365	370	375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp Thr	380	385	390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu Phe			

395	400	405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala	
410	415	420
Val Glu Lys Val	Thr Gln His Ile His Gly Leu Ser Gly Lys Lys	
425	430	435
Asp Gly Leu Val	Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe	
440	445	450
Thr His Leu Gly	Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr	
455	460	465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu	
470	475	480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg	
485	490	495
Thr His Leu Leu	Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val	
500	505	510
Gly Glu Leu Ala	His Gly Arg Phe Ser Ala Lys Met Asp His Leu	
515	520	525
Val Cys Phe Leu	Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly	
530	535	540
Leu Pro Ala Ser	His Met Glu Leu Ala Gln Glu Leu Met Glu Thr	
545	550	555
Cys Tyr Gln Met	Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu	
560	565	570
Ile Val His Phe	Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val	
575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr	
590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys	
605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe	
620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln	
635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe	
650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp	
665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala	
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccgggccg gccgggctgc gagcgccctgc 50
cccattgcgc gccgcctctc cgcacgatgt tcccctcgcg gaggaaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150
ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggcoctc cccgtgcctg 300
 cccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
 cccaccgctt ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450
 gcaccacatc tacgtgtctca accagggtgga ccacttcagg ttcaaccggg 500
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550
 attgccatgc acgacgttga cctgtccct ctcaacgagg agctggacta 600
 tggctttcct gaggtgtggc ccttcacgt ggcctccccg gagctccacc 650
 ctctctacca ctacaagacc tatgtcggcg gcacctgtct gctctccaag 700
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750
 ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
 ttttcgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850
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 acaggagcag ttcaagggtg acaggaggagg aggcctgaac actgtgaagt 950
 accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgact 1000
 gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050
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 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150
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 ggccgccaag gcaggcttg gctgggccag gacacgtggg gtgcctggga 1250
 cgctgcttgc catgcacagt gatcagagag aggctggggt gtgtcctgtc 1300
 cgggaccccc cctgccttcc tgctcaccct actctgacct ccttcacgtg 1350
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400
 cctactctga cctccttcac gtgccaggc ctgtgggtag tggggagggc 1450
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17

Met	Phe	Pro	Ser	Arg	Arg	Lys	Ala	Ala	Gln	Leu	Pro	Trp	Glu	Asp	1	5	10	15
Gly	Arg	Ser	Gly	Leu	Leu	Ser	Gly	Gly	Leu	Pro	Arg	Lys	Cys	Ser	20	25	30	
Val	Phe	His	Leu	Phe	Val	Ala	Cys	Leu	Ser	Leu	Gly	Phe	Phe	Ser	35	40	45	
Leu	Leu	Trp	Leu	Gln	Leu	Ser	Cys	Ser	Gly	Asp	Val	Ala	Arg	Ala	50	55	60	
Val	Arg	Gly	Gln	Gly	Gln	Glu	Thr	Ser	Gly	Pro	Pro	Arg	Ala	Cys	65	70	75	
Pro	Pro	Glu	Pro	Pro	Pro	Glu	His	Trp	Glu	Glu	Asp	Ala	Ser	Trp	80	85	90	
Gly	Pro	His	Arg	Leu	Ala	Val	Leu	Val	Pro	Phe	Arg	Glu	Arg	Phe	95	100	105	
Glu	Glu	Leu	Leu	Val	Phe	Val	Pro	His	Met	Arg	Arg	Phe	Leu	Ser	110	115	120	
Arg	Lys	Lys	Ile	Arg	His	His	Ile	Tyr	Val	Leu	Asn	Gln	Val	Asp	125	130	135	
His	Phe	Arg	Phe	Asn	Arg	Ala	Ala	Leu	Ile	Asn	Val	Gly	Phe	Leu				

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val	Asp
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu	Ala
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr	His
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln	His
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp	Gly
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly	Leu
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr	Phe
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys	Arg
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu	Gly
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala	Leu
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu	Asp
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser	
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctcttctg ccaactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200
tgccatgacc tgcagccaag ccagccccg tggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

gggacccatg cggccgtgac ccccggtcc ctagaggccc agcgagccg 50
cagcggacaa aggagcatgt ccgcgccggg gaaggcccg cctccggccg 100
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150
ggctccgggg cggcccgtta ggccagtgcg ccgcgcgctcg ccccgagggc 200
cccgggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgagc 250
cgccgctggt gctgccgctc tcgctgttag cgctgctgc gctgctggga 300
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tgggcgggcc cgaggggctg gcagggcggc gggcgccgc gagggcaagg 400
tggtgtgcag cagcctggaa ctgcgcgagg tctgcccc agatactctg 450
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggtaagtct ccttgaaaga ttggacctcc 550
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600
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atttgttttc ttcattatct caaggaactt ttgattatct tgcgtcatta 750
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctgggtaa aggagaagaa catcacggt cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
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 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050
 gatgggagaa tagttgaaac cgatgaatcg caaggatatt ttgttgaaaa 1100
 gaacatgatt cacaactgct ccttgattgc aagtgccta accatttcta 1150
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 ggcccagaac attggcaggc attactgcat atctgcagtg tacgcggaac 1350
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400
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 ccttattaaa agattttttt ttgcaggaag ataggtatta ttgcttttgc 2150
 tactgtttta aagaaaacta accaggaaga actgcattac gactttcaag 2200
 ggccctaggc atttttgcct ttgattccct ttcttcacat aaaaatatca 2250
 gaaattacat ttataactg cagtgggtata aatgcaaata tactattgtt 2300

acatgtgaaa aaatatttatt tgacttaaaa gtttatttat ttgttttttt 2350
 gtccttgatt ttaagacaat aagatgtttt catgggcccc taaaagtatc 2400
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 tcaataatat cacaacaat attccagtca ttttaatggc tgcataataa 2800
 ctgatccaac aggtgttagg tgttctgggt tagtgtgagc actcaataaa 2850
 tattgaatga atgaacgaaa aaaaaaaaaa aaa 2883

<210> 24
 <211> 616
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-33
 <223> Signal peptide.

<220>
 <221> TRANSMEM
 <222> 13-40
 <223> Transmembrane domain (type II).

<400> 24
 Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
 1 5 10 15
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
 20 25 30
 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
 35 40 45
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
 50 55 60
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
 65 70 75
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
 80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe		
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val		
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr		
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu		
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu		
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys		
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu		
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala		
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg		
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile		
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met		
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly		
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys		
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu		
590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr		
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Ser

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 <212> DNA
 <213> Artificial

 <220>
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 <222> 1-24

<223> Synthetic construct
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 <210> 26
 <211> 24
 <212> DNA
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 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.
 <400> 26
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 <211> 50
 <212> DNA
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 <220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.
 <400> 27
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 <211> 683
 <212> DNA
 <213> Homo sapiens
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 ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100
 gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
 aaaaagaaaa cattcgtctt ttgggagAAC agattatTTT gactgagcaa 200
 cttgaagcag aaagagagaa gatgttattg gcaaaaggat ctcaaaaatc 250
 atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300
 gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350
 actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400
 ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
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 tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

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<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens
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 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

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 20 25 30
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
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<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

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 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgc 150
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg ggggtcccca 200
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
 140 145 150
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
				215					220					225	
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
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<210> 32
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 <212> DNA
 <213> Homo sapiens

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taatataaaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
			20						25					30
Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
			35						40					45
His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
			50						55					60
Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
			65						70					75
Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
			80						85					90
Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
			95						100					105
Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
			110						115					120
Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
			125						130					135
Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
			140						145					150
Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
			155						160					165
Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
			170						175					180
Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
			185						190					195
His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
			200						205					210
Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
			215						220					225
Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
			230						235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
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<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
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 <212> DNA
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<220>
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 <223> Synthetic construct.

<400> 37
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<210> 38
 <211> 39
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<220>
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 <223> Synthetic construct.

<400> 38
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<210> 39
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 <212> DNA
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<220>
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 <223> Synthetic construct.

<400> 39
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<210> 40
 <211> 2084
 <212> DNA
 <213> Homo sapiens

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tgccagaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300
cctccacttc gtacttctgt atagaactaa cagcaaaaag gcgttaaaca 1350
gcaagtgtca tctacatcct agccttttga caaattcatc tttcaaaagg 1400
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggttttc 1500
tttcttacia tttttggcca tctgaggca tttactaagt agccttaatt 1550
tgtattttag tagtattttc ttagtagaaa atatttggtg aatcagataa 1600
aactaaaaga tttcaccatt acagccctgc ctcataacta aataataaaa 1650
attattccac caaaaaattc taaaacaatg aagatgactc tttactgctc 1700
tgctgaagc cctagtacca taattcaaga ttgcattttc ttaaatgaaa 1750

attgaaaggg tgctttttaa agaaaatttg acttaaagct aaaaagagga 1800
catagcccag agtttctggt attgggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agcttcttta aaagtcttca 2000
aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tgggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu	
				200					205					210	
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn	
				215					220					225	
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe	
				230					235					240	
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu	
				245					250					255	
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser	
				260					265					270	
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu	
				275					280					285	
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser	
				290					295					300	
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu	
				305					310					315	
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu	
				320					325					330	

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100
 cccctaccgc cgtgcaaaag gaggaggcgc ggcaagaçgt ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gtcctctgag gagatgtatg cttactctct 250
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgatg tgctgtccc cagtttctct gatagtgacc ctgcagcaat 500
 tattcatgac tttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

ggaactgcta tctgatgccc ctcaatactt ctattgttat gcctccaaaa 600
 aatctggtag agctcttttg caaactggcg agtggcagat atctgcctca 650
 aacttatgtg gttcgagaag acctagtgc tgtggaggaa attcgtgatg 700
 ttagtaacct tggcatcttt atttaccac tttgcaataa cagaaagtcc 750
 ttccgccttc gtcgcagaga cctcttgctg ggtttcaaca aacgtgccat 800
 tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850
 ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
 agaagtcaga gatttacaat atgactttta cattaagggt tatgggatac 950
 tcaagatatt tactcatgca ttactctat tgcttatgct ttaaaaaaag 1000
 gaaaaaaaaaaa aaactacta accactgcaa gctcttgtca aatttttagtt 1050
 taattggcat tgcttgtttt ttgaaactga aattacatga gtttcatttt 1100
 ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
 cctaacatcc tgacaataaa ttccatccgt tgtttttttt gtttgtttgt 1200
 tttttctttt cctttaagta agctctttat tcatcttatg gtggagcaat 1250
 tttaaaattt gaaatatttt aaattgtttt tgaacttttt gtgtaaaata 1300
 tatcagatct caacattggt ggtttctttt gtttttcatt ttgtacaact 1350
 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttctttctca ctactatctg tattgtggaa tgcacaaaat 1500
 tgtgtaggtg ctgaatgctg taaggagttt aggttgatatg aattctacaa 1550
 ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43
 <211> 263
 <212> PRT
 <213> Homo sapiens

<400> 43
 Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
 1 5 10 15
 Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
 20 25 30
 Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
 35 40 45
 Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-20
 <223> Synthetic construct.

 <400> 45
 gggaactgct atctgatgcc 20

 <210> 46
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 46
 caggatctcc tcttgcagtc tgcagc 26

 <210> 47
 <211> 28
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-28
 <223> Synthetic construct.

 <400> 47
 cttctcgaac cacataagtt tgaggcag 28

 <210> 48
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 48
 cacgattccc tccacagcaa ctggg 25

 <210> 49
 <211> 1969
 <212> DNA
 <213> Homo sapiens

 <400> 49
 ggaggagggga gggcgggcag ggcagagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100
cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150
gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
ccgagcctcc cgccaccctg gaccccggcc ctccagccca catcgatggg 350
gccccagccc acaaccctgg ggggcccatc acccccacc aacttcctgg 400
atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450
ggctccctgg cttttctgct gatgttcacg gtctgtgccg cggtcacac 500
ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550
agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600
gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
ctcccgagcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700
ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750
ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800
agtccaggga catggggctc cagtggagac accagaggcg caggaggagc 850
ctgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900
gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950
tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000
agtcctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050
ccccgtgtat gaaaaggcct tcagccctga ctgcttcctg aactccctc 1100
cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150
cagaaatgct ggtccccggt gccccggagg aatcttacca agtgccatca 1200
tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250
tgacaaagtg agggagggca cgtgtccctg tgacagccag gataaaacat 1300
ccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaac 1350
tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
aatactgctc ttaattttcc tgaagggtggc cccctgttcc tagttggtcc 1450
aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500

caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550
 gatcagggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
 agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
 ggggctgggg aagggtttct gacgcccagc ctggagcagg ggggccctgg 1700
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
 gtcagtcttc gacagggagc ctgggctccg tctgtcttta gggaggctct 1800
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
 1 5 10 15
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	170	175	180
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	185	190	195
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	200	205	210
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	215	220	225
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	230	235	240
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	245	250	255
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	260	265	270
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			275	280	

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350
 caaagaggcc ggaggggag ctggctctaa agtcagttag gcccttggcc 400
 aaggagaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
 acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650
 ccttgagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800
 caacactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtg 950
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050
 agtggtggca gcagtgga cagtgggtggc agcagaggtg acagcggcag 1100
 tgagtctcc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150
 ggagcggcgg aggaaatgga cataaaccgg ggtgtgaaaa gccagggaat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300
 gaggctctgg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcac 1500
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550
 cctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600
 aaataaacct tagctgcccc acaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
 <211> 440
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
 1 5 10 15
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
 20 25 30
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr 65 70 75		
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly 80 85 90		
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala 95 100 105		
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val 110 115 120		
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val 125 130 135		
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile 140 145 150		
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro 155 160 165		
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser 170 175 180		
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln 185 190 195		
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly 200 205 210		
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln 215 220 225		
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly 230 235 240		
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser 245 250 255		
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly 260 265 270		
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser 275 280 285		
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser 290 295 300		
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly 305 310 315		
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His 320 325 330		
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly 335 340 345		

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
 350 355 360
 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
 365 370 375
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
 380 385 390
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
 395 400 405
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
 410 415 420
 Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
 425 430 435
 Ser Ser Arg Ile Pro
 440

<210> 53
 <211> 3580
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaccggtccc tccggtcctg gatgtgcgga ctctgctgca gcgagggctg 50
 caggcccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100
 ctttgctgac catgttggtc ccttgctgga atattaccgg gacatcttca 150
 ctctcctgct gcgcctgcac cggagcttgg tgttgctcga ggagagtgag 200
 gggaagatgt gtttcttgaa caagctgctg ctacttgctg tcttgggctg 250
 gcttttccag attccacag tccctgagga cttgttcttt ctggaagagg 300
 gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350
 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400
 catcggagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450
 gacggagtgg gggcttcatt aggaaaatca cccccaccac taccaccagc 500
 ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550
 ccaggccttt ttccacaacc agccgccctc cttgcgccgg accgtagagt 600
 tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650
 ctggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700
 ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750
 tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccctggggct gtgcgggcgc tgcttccaga 850
 ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900
 ttgcaacaga gaaagcctgt gcttggctgt cagccaacat cacagcactg 950
 atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000
 tctgaacct gctgcccggg gggagcggag gggctgctcc cgcgccctgac 1050
 gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100
 agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150
 gccagttcct gtgcccacct gctgagcagc atctggcaaa gtgctctgtg 1200
 gagttagctt ccctcctcgt tgcagatcaa attcctatcc tagggcccc 1250
 ggcacagtac aggctggaga gagggcaggc tcgaaggctt ctgcacatgc 1300
 tgctttcctt gtggaaggaa gactttcagg ggccgggttc gctgcagctg 1350
 ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400
 gtgggacttg ctgctattct tgctacggga gctggtggag aagggtctga 1450
 tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500
 tggccagggg actttgctga agaattagca acactgtcta atctgtttct 1550
 agccgagccc cacctgccag aaccccagct aagagcctgt gagttggtgc 1600
 agccaaaccg gggcactgtg ctggcccaga gctagggctg agaagtggcc 1650
 ctgccttggg cattgcacca gaaccctgga ccccccgcctc acgaggaggc 1700
 ccaagtgccc aatgcagacc ctactgggtt ggggtgtagc tgggtctaca 1750
 gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgca 1800
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 <212> PRT
 <213> Homo sapiens

<400> 54

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Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala	
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<212> DNA
<213> Homo sapiens

<400> 55
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<213> Homo sapiens

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Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
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 <212> DNA
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<400> 57

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 <211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
 365 370 375
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
 395 400 405
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
 410 415 420
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
 425 430 435
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp	
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile	
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg	
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys	
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile	
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly	
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu	
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr	
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr	
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met	
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr	
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys	
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His	
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn	
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr	
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro	
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg	
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro	
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtag cctgtcgctg gaggc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccctaaag cccagggtccg gtacagcgctc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgaggagctg ggtcgctcatg atccggaccc cattgtcggc ctctgcccatt 50
cgctgtctcc tcccaggctc ccgcggccga ccccgcgca acatgcagcc 100
cacgggcccgc gaggggtccc gcgcgctcag ccggcggtat ctgcggcgctc 150
tgctgtctct gctactgctg ctgctgctgc ggcagcccgt aaccgcgcgcg 200
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250
cctcttcacc acgccgggtg tcccagcgc cctcactacc ccaggcctca 300
ctacgccagg caccctcaaa accctggacc ttgggggtcg cgcgcaggcc 350

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgccccaggt 400
 cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
 tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
 gccagttct ggtagcctc cgtctcatgc cagtcccagg accagactgc 550
 cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600
 cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650
 caaaagctgg cctgcctcat tggcgtgnag ggtgggtcact cactggacag 700
 cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750
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 agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850
 agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
 catcgacac cttgataaga agggctcctgg aagtgtctca ggctcctgtg 950
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 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtga 1050
 cactgtccat ggggggtgctg cagtgaacc tgcttgctaa cgtgtccact 1100
 gtggcagatc actttgacca catcaggga gtcattggat ctgagttcat 1150
 cgggattggg ggaaattatg acgggactgg ccggttccct caggggctgg 1200
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 cttcagacaa gtggaaaagg tgagagagga gagcaggggc cagagccccg 1350
 tggaggctga gtttccatat gggcaactga gcacatccg ccactcccac 1400
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaccaat cgggtcccct ggaggtcctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgctgacaca gtcggtcccc gcagagggtca ctgtggcaaa gcctcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 196, 386
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
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Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20				25						30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35				40						45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50				55						60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65				70						75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80				85						90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95				100						105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110				115						120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125				130						135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140				145						150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155				160						165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170				175						180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185				190						195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200				205						210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215				220						225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230				235						240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245				250						255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480

Thr Phe Thr Gln Trp Leu Cys
485

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 66
 ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
 <211> 1564
 <212> DNA
 <213> Homo sapiens

<400> 67
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 aacaccacaca gatccctcta tgactgcaat gtgagggtgc cggctttgct 100
 ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
 cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
 tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
 tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
 gcccatgcc a gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
 agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
 atctacctgt ccgtggtggg tgccctgttg ctctacatgg ccttcctgat 450
 gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
 acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
 tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaagggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650
 atcggcacia gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
 ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800
 ctcttctccc ctaactttag aaatgttgta cttggctatt ttgattaggg 850
 aagaggggatg tggctctga tctctgttggt cttcttgggt ctttgggggt 900
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
 ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
 cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050
 ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
 gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150
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 ctctccccag tgtccacagt cactgagcca gacggtcgggt tggaacatga 1400
 gactcgagggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450
 gcctcttgct cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500
 tcctcttgct ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
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 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
				170					175					180	

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
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 agttcatagg gtcctgggtc cccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggctctccc 150
 tccctttgca ttcccacccc tccgggcttt gcgtcttcct ggggaccccc 200
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
 gcatgtgctg cccagtagcc cgctgcaata atggcatctg tatcccagtt 600
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gaccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
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tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
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gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
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ttatacaaat aacctacatg ccagatttct attcaacggt agagtttaac 1400
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aatgaaaac atggagcatt gttaatttac aacagaaaat 1500
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac ttttttttca aaattttagt tttacctgta attaataaga 1700
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aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150
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 aaatataagt aggataactt gtaaacctg catattgcta atctatagac 2500
 accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550
 aactcagttc taaatacttt gtctggagca caaaacaata aaaggttatc 2600
 ttatagtcgt gactttaaac tttttagtag cacaattcac tttttagttt 2650
 tcttttactt aaatcccatc tgcagtctca aatttaagtt ctcccagtag 2700
 agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
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 caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850
 tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttctt 2900
 atataacaat tattatattt acaatttggg ttctgcaata tttttcttat 2950
 gtccaccctt ttaaaaatta ttatttgaag taatttatat acaggaaatg 3000
 ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
 gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
 taagataaaa tctattaaat ttttctctc taaaaactga aaaaaaaaaa 3150
 aaaaaaaaaa aaaaaaaaaa 3170

<210> 70
 <211> 259
 <212> PRT
 <213> Homo sapiens

<400> 70
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 Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
 20 25 30
 Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
 35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 tggcctccca aagtgttggg attacaggcg tgagccaccg cgccccgccca 100
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatattcc 150
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250
 atattttagt aattcatatg ttttagatta taggttttaa cataacttggtg 300
 aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350
 ggatttggtc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
 tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
 tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
 ctcaagcccc caacatccca gtcctcagtc ctcagtcatc ttgacttcaa 600
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
 agcaccagag ccaggcagtc actgttcctc ctctgggtt ggagtccttt 700
 cttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
 tgtgaacaag cttttgcagc ttcccagcac gaccattgaa aatatctctg 800
 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
 atacccccag cttctaagat ccagcttct gcagtggaaa tgcctgggtc 900
 agcagatgtc acaggattaa atgtgcagtt tggggctctg gaatttgggt 950
 cagaaccttc tctctctgaa tttggatcag ctccaagcag tgaaaatagt 1000
 aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100
 ccgtcattac ctctgcagt ctgacaagct catcactgaa ttctgctagt 1150
 ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200
 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
 tgaatggaca tgggtgggtg cgaagtcagc agacactaga cagtaagtat 1300
 agcagcaagc tactcttgtc atggctgggt ccaaccaaac agaggaagag 1350
 gatagctcac gtgatgtgga aaacaccagt tgggtcaatgg ctcattcgtt 1400
 aaaaagcagc ctttttgctt ttttgttttt ggaccagggtg ttggctgtgg 1450
 tgttattaga aatgtcttaa ccacagcaag aaggagggtg tggctctcata 1500
 ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagtatgcat 1550
 tttaaagatg cttgggccag gcgggggtggc tgatgcccat aatcccagtg 1600
 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700
 gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
 ctgaaaaga 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72
 Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
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 Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
 20 25 30
 Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
 35 40 45
 Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
 50 55 60
 Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
 65 70 75
 Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
 80 85 90
 Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
 95 100 105
 Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
 110 115 120
 Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
 125 130 135
 Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
 140 145 150
 Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
 155 160 165
 Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 170 175 180
 Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
 185 190 195
 Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
 200 205 210
 Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 215 220 225

Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-26

<223> Synthetic construct.

<400> 73

aattcatggc aaatatttcc cttccc 26

<210> 74

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 74

tggtaaactg gcccaaactc gg 22

<210> 75

<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac cgcgccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtggg acaaagcctg gggctgggcg ggggccatgg cgctgccatc 50
ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100
tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200
caccgacggc cccccggcca cccccgccta ctgggacggc gagaaggagg 250
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gggcacgtgt ggaccgaccg gcacgtggag gaggtcaac aggtggtgca 350
ctgggacggc cagccgcccg ggggtcccga cgaccgcgcg gaccgcctgc 400
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cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750
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aactgcaa at agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
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ccaccctgc ggcttttgc caggggtggc cctgccacc cctggcaca 1300
ccaaaatccc actgatgcc atcatgccct cagacccttc tgggctctgc 1350
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cagccccaaa actggggtca gcctcagggc aggagtcca ctctccagg 1450
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ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950
caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala	Pro Ala Leu Leu Thr	Cys Val Asn Arg Gly His
80	85	90
Val Trp Thr Asp	Arg His Val Glu Glu Ala Gln Gln Val Val	His
95	100	105
Trp Asp Arg Gln	Pro Pro Gly Val Pro His Asp Arg Ala Asp	Arg
110	115	120
Leu Leu Asp Leu	Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly	Pro
125	130	135
Leu Phe Leu Arg	Asp Arg Val Ala Val Gly Ala Asp Ala Phe	Glu
140	145	150
Arg Gly Asp Phe	Ser Leu Arg Ile Glu Pro Leu Glu Val Ala	Asp
155	160	165
Glu Gly Thr Tyr	Ser Cys His Leu His His His Tyr Cys Gly	Leu
170	175	180
His Glu Arg Arg	Val Phe His Leu Thr Val Ala Glu Pro His	Ala
185	190	195
Glu Pro Pro Pro	Arg Gly Ser Pro Gly Asn Gly Ser Ser His	Ser
200	205	210
Gly Ala Pro Gly	Pro Asp Pro Thr Leu Ala Arg Gly His Asn	Val
215	220	225
Ile Asn Val Ile	Val Pro Glu Ser Arg Ala His Phe Phe Gln	Gln
230	235	240
Leu Gly Tyr Val	Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu	Leu
245	250	255
Val Thr Val Leu	Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr	Glu
260	265	270
Tyr Ser Asp Gln	Lys Ser Gly Lys Ser Lys Gly Lys Asp Val	Asn
275	280	285
Leu Ala Glu Phe	Ala Val Ala Ala Gly Asp Gln Met Leu Tyr	Arg
290	295	300
Ser Glu Asp Ile	Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys	Glu
305	310	315
Arg Ala Glu Leu	Ala His Ser Pro Leu Pro Ala Lys Tyr Ile	Asp
320	325	330
Leu Asp Lys Gly	Phe Arg Lys Glu Asn Cys Lys	
335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78

cgccggaggc agcggcggcg tggcgagcg ggcacatggc cgttgtctca 50
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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200
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cactgccaag gactactgga tgttcaaact cgcgaactcc tccagcccag 300
ccaccgggga ggacctgag ggctcagaca tcctgaacta ctttgagagc 350
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 gccagtgccaa aaaccagcc atgggctctt tgcaacctcc cagctgcgct 1850
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 ccactaacca gactggaaaa ccagaaaaga tgggccttcc atgaatgctt 2050
 cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100
 ggctggggtt ttcaaaaaaa gagggatcct catgacctgg tggcttatgg 2150
 cctgggtcaa gatgaggggtc ttccagtgtt cctgtttaca acatgtcaaa 2200
 gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79
 <211> 475
 <212> PRT
 <213> Homo sapiens

<400> 79
 Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
 1 5 10 15
 Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
 20 25 30
 Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
 35 40 45
 Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
 50 55 60
 Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
 65 70 75
 Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
 80 85 90
 Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
 95 100 105

Tyr Leu Ala Val	Ala Ser Thr Val Pro	Ser Met Leu Cys Leu Val
110	115	120
Ala Asn Phe Leu	Leu Val Asn Arg Val	Ala Val His Ile Arg Val
125	130	135
Leu Ala Ser Leu	Thr Val Ile Leu Ala	Ile Phe Met Val Ile Thr
140	145	150
Ala Leu Val Lys	Val Asp Thr Ser Ser	Trp Thr Arg Gly Phe Phe
155	160	165
Ala Val Thr Ile	Val Cys Met Val Ile	Leu Ser Gly Ala Ser Thr
170	175	180
Val Phe Ser Ser	Ser Ile Tyr Gly Met	Thr Gly Ser Phe Pro Met
185	190	195
Arg Asn Ser Gln	Ala Leu Ile Ser Gly	Gly Ala Met Gly Gly Thr
200	205	210
Val Ser Ala Val	Ala Ser Leu Val Asp	Leu Ala Ala Ser Ser Asp
215	220	225
Val Arg Asn Ser	Ala Leu Ala Phe Phe	Leu Thr Ala Thr Ile Phe
230	235	240
Leu Val Leu Cys	Met Gly Leu Tyr Leu	Leu Leu Ser Arg Leu Glu
245	250	255
Tyr Ala Arg Tyr	Tyr Met Arg Pro Val	Leu Ala Ala His Val Phe
260	265	270
Ser Gly Glu Glu	Glu Leu Pro Gln Asp	Ser Leu Ser Ala Pro Ser
275	280	285
Val Ala Ser Arg	Phe Ile Asp Ser His	Thr Pro Pro Leu Arg Pro
290	295	300
Ile Leu Lys Lys	Thr Ala Ser Leu Gly	Phe Cys Val Thr Tyr Val
305	310	315
Phe Phe Ile Thr	Ser Leu Ile Tyr Pro	Ala Val Cys Thr Asn Ile
320	325	330
Glu Ser Leu Asn	Lys Gly Ser Gly Ser	Leu Trp Thr Thr Lys Phe
335	340	345
Phe Ile Pro Leu	Thr Thr Phe Leu Leu	Tyr Asn Phe Ala Asp Leu
350	355	360
Cys Gly Arg Gln	Leu Thr Ala Trp Ile	Gln Val Pro Gly Pro Asn
365	370	375
Ser Lys Ala Leu	Pro Gly Phe Val Leu	Leu Arg Thr Cys Leu Ile
380	385	390
Pro Leu Phe Val	Leu Cys Asn Tyr Gln	Pro Arg Val His Leu Lys

	395		400		405
Thr Val Val Phe	Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser			
	410	415		420	
Leu Leu Gly Leu	Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu			
	425	430		435	
Tyr Gly Pro Lys	Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly			
	440	445		450	
Val Val Met Ser	Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser			
	455	460		465	
Ala Cys Ser Thr	Leu Leu Val His Leu	Ile			
	470	475			

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgccggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgcctgctg tcaccaagag 50
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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgacctg ggggctcaat cggaccctga 250
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gccaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
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ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
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 aaaacacgac ccacacgagg acctcgcatt aaagtatttt cggaaaaaaa 1800
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
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 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcgcga gggctctgaat ttctgtctgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcc a ttttcttggtg gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga aggggggttc ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500
 tgtctgacaa tgggccctgc ttgggatata gaaaaccaa ccagccctac 550
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ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatctgctt caccagtggg accacaggtg accccaaagg 1050
agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100
aatgtgtgga gcatgcttat gagccactc ctgatgatgt ggccatatcc 1150
tacctccctc tggctcatat gtttgagagg attgtacagg ctgttgtgta 1200
cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctg 1250
ctgacgacat gaagactttg aagccacat tgtttccgc ggtgcctga 1300
ctccttaaca ggatctacga taaggtaaa aatgaggcca agacaccctt 1350
gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400
aaaagggat catcaggcat gatagtttct gggacaagct catctttgca 1450
aagatccagg acagcctggg cggaagggtt cgtgtaattg tctactggagc 1500
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aatTTTTgta cagggggaga gcttacggtc atccttagta ggagtgggtg 2000
ttcctgacac agatgtactt ccctcatttg cagccaagct tgggggtgaag 2050
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ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250
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 aaaaactatt cttacatttg ttttgccttt cctcctattt tttttaacc 2400
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 ctgcgtaaat taaattgtgt actgaaggga aaagtttgat cataccaaac 2900
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 cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050
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 acaggcaagc aagatgcca cacaacaggc ttattttctg tgaaggaacc 3200
 aactgatctc cccaccctt ggattagagt tctgctcta ccttaccac 3250
 agataacaca tggtgtttct acttgtaa atgttaagtctt taaaataaac 3300
 tattacagat aaaaaa 3316

<210> 86
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 86
 Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

Gly Ser Pro His	Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser	35	40	45
Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile		50	55	60
Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys		65	70	75
Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg		80	85	90
Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val		95	100	105
Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn		110	115	120
Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu		125	130	135
Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu		140	145	150
Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys		155	160	165
Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His		170	175	180
Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala		185	190	195
Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr		200	205	210
Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu		215	220	225
Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile		230	235	240
Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu		245	250	255
Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro		260	265	270
Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu		275	280	285
Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe		290	295	300
Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys		305	310	315
Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr				

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
				725					730					735

His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 gcccgagcgg ggcccggggc ccctaagcca ttcctgaagt catgggctgg 100
 ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 cagggggcgt gcttttcctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctgcggcagc catcagtga gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
 gaggcagtgg tccccggcgg gtccctggacg tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
 ccgggagcag ggccggggc tccatgtcat tgcctcaac caggccacgg 550
 gccacgtgat ggcaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
 gaggccatgg tgctattcct caacatggta gcgcccggcc gagggtcat 650

ctgcactgtc aaggatgagg gctccttcca cctcaaggac acagccaagg 700
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 gacacatggg cttctgtggg acgaaaagga ggtcctgtct tcggggagaa 800
 acatttctaag tcacctgccc tctcttctctg gggggaccca gtctgtctga 850
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 gacacagagc tgaaccgtcg ccgccggcgc ttctgcagca aagttgaggg 950
 ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
 ctgaccact cccagacaac aaggctctca atgtgcctgt ggctgtcatt 1050
 gcagggaacc gaccaatta cctgtacagg atgctgcgct ctctgctttc 1100
 agcccagggg gtgtctctc agatgataac agttttcatt gacggctact 1150
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 ttctggaaga ggacctggac attgctgtgg attttttcag tttctgagc 1350
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 ctggaatgac caggggtatg aacacacggc tgaggacca gactactgt 1450
 accgtgtgga gaccatgcct gggctgggct ggggtgctcag gaggtccttg 1500
 tacaaggagg agcttgagcc caagtggcct acaccgaaa agctctggga 1550
 ttgggacatg tggatgcgga tgcctgaaca acgccggggc cgagagtgca 1600
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 cttagacact ggaccaggcc tcctctcagc cttctctttg tccagatttc 2650
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
 Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
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 Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
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 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Leu Asn Gln Ala Thr Gly His Val Met	Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met	Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys	Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys	Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly	Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val	Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly	Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu	Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg	Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser	Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro	Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn	Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala	Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr	Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly	Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln	His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu	Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val	Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu	Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr	Glu His Thr Ala Glu			

425										430					435				
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly					
				440					445					450					
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys					
				455					460					465					
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg					
				470					475					480					
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val					
				485					490					495					
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly					
				500					505					510					
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val					
				515					520					525					
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala					
				530					535					540					
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu					
				545					550					555					
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr					
				560					565					570					
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp					
				575					580					585					
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp					
				590					595					600					
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe					
				605					610					615					
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro					
				620					625					630					
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu					
				635					640					645					
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr					
				650					655					660					

<210> 89
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 89

gatggcaaaa cgtgtgtttg acacg 25
 <210> 90
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 90
 cctcaaccag gccacgggcc ac 22

 <210> 91
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 91
 cccaggcaga gatgcagtac aggc 24

 <210> 92
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 92
 cctccagtag gtggatggat tggctc 26

 <210> 93
 <211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 93
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 <210> 94
 <211> 3037
 <212> DNA
 <213> Homo sapiens

<400> 94

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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95

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Val	Gly	Cys	Tyr	Val	Ala	Gly	Ile	Ile	Pro	Leu	Ala	Val	Asn	Phe	20	25	30	
Ser	Glu	Glu	Arg	Leu	Lys	Leu	Val	Thr	Val	Leu	Gly	Ala	Gly	Leu	35	40	45	
Leu	Cys	Gly	Thr	Ala	Leu	Ala	Val	Ile	Val	Pro	Glu	Gly	Val	His	50	55	60	
Ala	Leu	Tyr	Glu	Asp	Ile	Leu	Glu	Gly	Lys	His	His	Gln	Ala	Ser	65	70	75	
Glu	Thr	His	Asn	Val	Ile	Ala	Ser	Asp	Lys	Ala	Ala	Glu	Lys	Ser	80	85	90	
Val	Val	His	Glu	His	Glu	His	Ser	His	Asp	His	Thr	Gln	Leu	His	95	100	105	
Ala	Tyr	Ile	Gly	Val	Ser	Leu	Val	Leu	Gly	Phe	Val	Phe	Met	Leu	110	115	120	
Leu	Val	Asp	Gln	Ile	Gly	Asn	Ser	His	Val	His	Ser	Thr	Asp	Asp	125	130	135	
Pro	Glu	Ala	Ala	Arg	Ser	Ser	Asn	Ser	Lys	Ile	Thr	Thr	Thr	Leu	140	145	150	
Gly	Leu	Val	Val	His	Ala	Ala	Ala	Asp	Gly	Val	Ala	Leu	Gly	Ala	155	160	165	
Ala	Ala	Ser	Thr	Ser	Gln	Thr	Ser	Val	Gln	Leu	Ile	Val	Phe	Val	170	175	180	
Ala	Ile	Met	Leu	His	Lys	Ala	Pro	Ala	Ala	Phe	Gly	Leu	Val	Ser	185	190	195	
Phe	Leu	Met	His	Ala	Gly	Leu	Glu	Arg	Asn	Arg	Ile	Arg	Lys	His	200	205	210	
Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	215	220	225	
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val				

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile		
290	295	300
Leu Ser Val Gly His Gln His		
305		

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
 gttgtgggtg aataaaggag ggcag 25

<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gttcatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
 ggatgatttc atctccatta gctgtgtg tctggctatg ttggtgggat 50

<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgccccctc tgctggccgc cctggtggcc tgcattcatc tcttgggctt 200
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gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400
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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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			20						25					30	
Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg	
			35						40					45	
Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg	
			50						55					60	
Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu	
			65						70					75	
Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe	
			80						85					90	
Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val	
			95						100					105	
Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu	
			110						115					120	
Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln	
			125						130					135	
Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg	
			140						145					150	
Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu	
			155						160					165	
Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys	
			170						175					180	
Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp	
			185						190					195	
Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu	
			200						205					210	
Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly	
			215						220					225	
Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser	
			230						235					240	

Glu Val Val Leu	Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr	245	250	255
Asn Glu Ile Gln	Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu	260	265	270
Pro Gln Glu Pro	Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val	275	280	285
Gly Gly Arg Gly	Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro	290	295	300
Gln Val Gln Ala	Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met	305	310	315
Glu Gly Pro Glu	Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu	320	325	330
Glu Glu Gln Glu	Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu	335	340	345
Arg Gly Glu Asp	Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser	350	355	360
Glu Thr Asp Lys	Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile	365	370	375
Asp Val Phe Asn	Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu	380	385	390
Leu Asp Gln Arg	Glu Lys Arg Asn His Thr Leu	395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102

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				20					25					30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	
				35					40					45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	
				50					55					60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	
				65					70					75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	
				80					85					90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	
				95					100					105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	
				110					115					120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	
				125					130					135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	
				140					145					150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	
				155					160					165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp	
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val	Asp His Cys Gly His Lys	
230	235	240
His Gly Pro His His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg	
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile Cys	
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe Cys	
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp	Gly Leu Val Gly Ala Ile	
485	490	495

Ala Tyr Ala Gly	Leu	Leu Gly Thr Ile	Glu	Leu Lys Leu Asp	Leu
	500		505		510
Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe		
	515		520		525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala		
	530		535		540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu	Phe		
	545		550		555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala		
	560		565		570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val		
	575		580		585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu		
	590		595		600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg		
	605		610		615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu		
	620		625		630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr		
	635		640		645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met		
	650		655		660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala		
	665		670		675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg		
	680		685		690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg		
	695		700		705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala		
	710		715		720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu		
	725		730		735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu		
	740		745		750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val		
	755		760		765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu		
	770		775		780
Thr Pro Phe Ser Gly	Pro Pro Thr Ser Gln	Ala Asp Leu Asp Tyr			

785										790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met		Gln	Glu	Glu	Phe	Arg	Gly				
				800											810				
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly		Pro	Leu	Thr	Val	Ala	Ala				
				815											825				
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala		Ala	Met	Val	Thr	Ala	Leu				
				830											840				
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu		Leu	His	Ala	Glu	Arg	Ile				
				845											855				
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu		Gln	Ser	Phe	Leu	Leu	Leu				
				860											870				
His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val		Thr	Thr	Pro	Gly	Pro	Phe				
				875											885				
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala		Trp	Ala	Leu	Met	Ala	Thr				
				890											900				
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln		Pro	Val	Phe	Pro	Ala	Ile				
				905											915				
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe		Pro	Glu	Gly	His	Gly	Ser				
				920											930				
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val		Gly	Ala	Asn	Thr	Phe	Ala				
				935											945				
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys		Pro	Leu	Leu	Leu	Leu	Trp				
				950											960				
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu		Arg	Lys	Arg	Gln	Gln	Pro				
				965											975				
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val		Arg	Pro	Glu	Glu	Glu	Glu				
				980											990				
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg		Asp	Ala	Pro	Gln	His	Phe				
				995											1005				
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu		Lys	Tyr	Leu	Phe	Ile	Leu				
				1010											1020				
Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu		Ala	Ala	Ser	Ile	Leu	Arg				
				1025											1035				
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe		Ala	Pro	Lys	Phe	Ile	Phe				
				1040											1050				
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser		Val	Gly	Leu	Leu	Leu	Gly				
				1055											1065				
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly		Ala	Val	Ser	Ser	Trp	Phe				
				1070											1080				

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 103
tgccgctgcc gccgctgctg ctgttgctcc tggcggcgcc ttggggacgg 50
gcagttccct gtgtctctgg tggtttgctt aaacctgcaa acatcacctt 100
cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaacgtggg ccagtggtgt gaccaaccac acgctgggtg 400
tcacctgggt ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
aaaaaatcgt gattaacttt atcacctca atatctcgga tgattctaaa 750
atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800
ccttaatgat cctcagcca gcgggaacct gaggccctc caggaggaag 850
aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900
gactctgaag aaaacacgga aggtacttct ctcaccagc aagagtcctt 950
cagcagaaca ataccccg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggaggggccc 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
 agccttctga ggggggatggg ctcgagagg agggctcttct atctagactc 1350
 tatgaggagc cggctccaga caggccacca ggagaaaatg aaacctatct 1400
 catgcaattc atggaggaat ggggggttata tgtgcagatg gaaaactgat 1450
 gccaacactt ccttttgcct tttgtttcct gtgcaaaca gtgagtcacc 1500
 cctttgatcc cagccataaa gtacctggga tgaaagaagt tttttccagt 1550
 ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
 cgtgtgtgat tggttcatgc atgtaggtct cttaacaatg atgggtgggcc 1650
 tctggagtcc aggggctggc cggttggtct atgcagagaa agcagtcaat 1700
 aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys	1	5	10	15
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu	20	25	30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr	35	40	45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser	50	55	60	
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu	65	70	75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His	80	85	90	
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105	
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120	
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150	
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165	

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile		170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys		185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys		200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val		215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro		230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu		245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser		260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys		275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys		290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser		305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu		320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp		335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro		350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr		365	370	375
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser		380	385	390
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly		395	400	405
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro		410	415	420
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly		425	430	435
Leu	Tyr	Val	Gln	Met	Glu	Asn										440		

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51

<223> Synthetic construct.

<400> 109

ggacgggcag ttccctgtgt ctctggtggt ttgcctaaac ctgcaaacaat 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

cggacgcgtg ggccggacgcg tgggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgtgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150
gctcctgggg ggccagatc atcgggggcc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250
cttcctgctg cgagcccgt ggggtgtctc ggccgcccac tgcttcagcc 300
acagagacct ccgactggc ctggtggtgc tgggcgcca cgtcctgagt 350
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400
ccccgactac caccatga ccacgcca cgacatctgc ctgctgcggc 450
tgaacggctc tgctgtcctg ggccctgcag tggggtgct gaggctgcca 500
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctgg 550
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ctcacggcct cgtttcctc tcgggcctct ggtgcggcga cccaagacc 800
cccacgtgt acacgcagg gtccgccttt gtggcctgga tctgggacgt 850
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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgtccag gcctggaatg ttccgtggct gggcccccac ggaagcctga 1000
tgttcagggg tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met	Gly	Leu	Gly	Leu	Arg	Gly	Trp	Gly	Arg	Pro	Leu	Leu	Thr	Val
1				5					10					15
Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
				35					40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60
Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90
His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105
Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120
Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135
Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150
Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165
Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180
Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195
Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
 275 280

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 112
 gacgtctgca acagctcctg gaag 24

<210> 113
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-44
 <223> Synthetic construct.

<400> 114
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
 gagctaccca ggcggctggt gtgcagcaag ctccgcgccg actccggacg 50
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150
 tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200

ggtcatcgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
 tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400
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 aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
 gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
 tgctggacaa gctgaaagcc tcagcccctt cgcggatcat caacctctcg 600
 tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
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 ctggccgtgg cggaggaact ggcggatgtt tccggaagt acttcgatgg 950
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 ggaggctttg ggctgaaagt gccgcctgg tgggcttaga ggctccctct 1050
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 ctggcactac ctgagccggg agaccagga ctggcggccg ccatgccccg 1200
 agtaggttct agggggcggt gctggccgca gtggactggc ctgcaggtga 1250
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 agaggggcca tctgatgctt ccctgggaa tctaaactgg gaatggccga 1350
 ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcggg 1400
 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450
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 gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
 ctgtctccca tgatggtgtg gtacagcgag ctgttgtctg gctatggcat 1600
 ggctgtgccg ggggtgtttg ctgaggcctt cctgtgccag agcccagcca 1650

gagagcaggt gcaggtgtca tcccaggttc aggcctctgca cggcatggag 1700

tggggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750

caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800

gctcattt 1808

<210> 116

<211> 331

<212> PRT

<213> Homo sapiens

<400> 116

Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
1 5 10 15

Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
20 25 30

Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45

Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60

Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75

Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90

Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105

Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
110 115 120

Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135

Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150

Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165

Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180

His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
185 190 195

Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
200 205 210

Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
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 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
 agcgccggct gctggggctg ctgaggcggg acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggccctg atgcggctgc 450
 aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
 agagtcaactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggt gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000
 ttccaacgcc tacctgtctc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgtctct taccatgact tcgtcagtga ctcagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac caaaactgg tgaccctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggg gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800
 gggagagggt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850
 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900
 ggcctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950
 acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000
 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
 tagcctgact cccagaactt taagaatttc tccccactgc cttctgtctc 2100
 agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser	Cys Ala Leu Ser Leu	Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp	Asn Lys Arg Met Ala	Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu	Ala Glu Ser Pro Asn	His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg	Pro Asn Ile Pro His	Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu	Cys Gln Thr Leu Gly	Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser	Leu Tyr Cys Ser Tyr	Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu	Gln Pro Ile Arg Lys	Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala	Leu Tyr His Asp Phe	Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg	Glu Leu Ala Glu Pro	Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly	Glu Lys Gln Leu Gln	Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp	Leu Lys Asp Thr Val	Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg	Ile Ala Ala Leu Thr	Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu	Tyr Leu Gln Val Val	Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro	His Phe Asp His Ala	Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met	Lys Ser Gly Asn Arg	Val Ala Thr Phe Met Ile	455	460	465
Tyr Leu Ser Ser	Val Glu Ala Gly Gly	Ala Thr Ala Phe Ile Tyr	470	475	480
Ala Asn Leu Ser	Val Pro Val Val Arg	Asn Ala Ala Leu Phe Trp	485	490	495
Trp Asn Leu His	Arg Ser Gly Glu Gly	Asp Ser Asp Thr Leu His	500	505	510
Ala Gly Cys Pro	Val Leu Val Gly Asp	Lys Trp Val Ala Asn Lys	515	520	525
Trp Ile His Glu	Tyr Gly Gln Glu Phe	Arg Arg Pro Cys Ser Ser			

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gacccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagatagggg gtctgggttt aagttcctgc tccatctcag gagcccctgc 50

tcccaccctt aggaagccac cagactccac ggtgtggggc caatcaggtg 100

gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgcg ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcaattatca tctattccac cgtgttctgg ctgattgggg 300
 ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
 gggcgctcgc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550
 gaccattgac ttcctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtctgt gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gcccttgac ccctggcctg tgggggtgcc tacacctgct 750
 gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcgtttcag tgtgcaggat gtcactacg tgcggggctg 850
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
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 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050
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 ggcagtgcct tggcgggtgg attcaaggca gttttgtagc acctgtaatt 1450
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 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
 ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggctgct 1600
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700

gtcttattct tgcccttccc ccaaccagtt tgtaatacaa acaataaaaa 1750

catgttttgt ttgttttta aaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe
1				5					10					15

Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
				170					175					180

Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195

Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210

Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225

Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	230		235		240									
Ile	Leu	Leu	Pro	Gln	Phe	Leu	Gly	Val	Leu	Leu	Thr	Leu	Leu	Tyr
			245						250					255
Ile	Thr	Arg	Val	Glu	Asp	Ile	Ile	Met	Glu	His	Ser	Val	Thr	Asp
			260						265					270
Gly	Leu	Leu	Gly	Pro	Gly	Ala	Lys	Pro	Ser	Val	Glu	Ala	Ala	Gly
			275						280					285
Thr	Gly	Cys	Cys	Leu	Cys	Tyr	Pro	Asn						
			290											

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100
ctctgtgggt tgctggcagc caccttgatc caagccaccc tcagtcccac 150
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300
ggtgaacacc gtctgaagc acatcatctg gctgaaggct atcacagcta 350
acatcctcca gctgcagggt aagccctcgg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500
tggacaccag tgcaagtggc cccaccgcgc tggtcctcag tgactgtgcc 550
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcct 600
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagtg ccatccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700
ggcatgtatg cagacctcct gcagctgggt aaggtgccc tttccctcag 750
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800
ccattcagct ctacctgggg gccaaagttgt tggactcaca gggaaaagggtg 850
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900
caacatcccg ttcagcctca tcgtgagtca ggacgtgggt aaagctgcag 950
tggtgctgtg gctctctcca gaagaattca tggtcctggt ggactctgtg 1000
cttctgaga gtgccatcg gctgaagtca agcatcgggc tgatcaatga 1050
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aggacactcc cgagtttttt atagaccaag gccatgcaa ggtggcccaa 1150
ctgatcgtgc tggaagtgtt tcctccagt gaagccctcc gccctttggt 1200
caccctgggc atcgaagcca gtcggaagc tcagttttac accaaagggtg 1250
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctggggg ccagtgatca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttgtg cttactccag cctccttgtg 1500
 gaaacccagc tctcctgtct ccagtggaag acttggtatgg cagccatcag 1550
 ggaaggctgg gtccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgctgtg gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala	1	5	10	15
Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile	20	25	30	35
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys	35	40	45	50
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser	50	55	60	65
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	65	70	75	80
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile	80	85	90	95
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	95	100	105	110
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	110	115	120	125
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	125	130	135	140
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	140	145	150	155
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu	155	160	165	170
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu	170	175	180	185
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu	185	190	195	200
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly	200	205	210	215
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu	215	220	225	

Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile	Lys
230	235		240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp	Ser
245	250		255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser	Leu
260	265		270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val	Ser
275	280		285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro	Glu
290	295		300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala	His
305	310		315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala	Asp
320	325		330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp	Thr
335	340		345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln	Leu
350	355		360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro	Leu
365	370		375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr	Thr
380	385		390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser	Asp
395	400		405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro	Asp
410	415		420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu	Leu
425	430		435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser	Leu
440	445		450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr	Lys
455	460		465
Asp Ala Leu Val	Leu Thr Pro Ala Ser	Leu Trp Lys Pro Ser	Ser
470	475		480
Pro Val Ser Gln			

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129

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 gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050
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 aaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
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 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	110	115	120
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	125	130	135
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	140	145	150
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	155	160	165
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	170	175	180
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	185	190	195
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	200	205	210
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	215	220	225
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	230	235	240
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	245	250	255
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	260	265	270
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	275	280	285
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	290	295	300
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	305	310	315
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	320	325	330
Ser	Phe	Leu	Met	Ser											335		

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

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 cttggcgctg gcggtactgg ccccgaggc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
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 ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800
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 ttctttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
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 aatcacatat tttaaaaaat ggttattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
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<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
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 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

	365		370		375
Leu Ser Gly Tyr	Ser 380	Leu Leu Pro Leu	Ser 385	Ser Glu Thr Phe	Lys 390
Asn Glu His Lys	Val 395	Lys Asn Leu His	Pro 400	Pro Trp Ile Leu	Ser 405
Glu Phe His Gly	Cys 410	Asn Val Asn Ala	Ser 415	Thr Tyr Met Leu	Arg 420
Thr Asn His Trp	Lys 425	Tyr Ile Ala Tyr	Ser 430	Asp Gly Ala Ser	Ile 435
Leu Pro Gln Leu	Phe 440	Asp Leu Ser Ser	Asp 445	Pro Asp Glu Leu	Thr 450
Asn Val Ala Val	Lys 455	Phe Pro Glu Ile	Thr 460	Tyr Ser Leu Asp	Gln 465
Lys Leu His Ser	Ile 470	Ile Asn Tyr Pro	Lys 475	Val Ser Ala Ser	Val 480
His Gln Tyr Asn	Lys 485	Glu Gln Phe Ile	Lys 490	Trp Lys Gln Ser	Ile 495
Gly Gln Asn Tyr	Ser 500	Asn Val Ile Ala	Asn 505	Leu Arg Trp His	Gln 510
Asp Trp Gln Lys	Glu 515	Pro Arg Lys Tyr	Glu 520	Asn Ala Ile Asp	Gln 525
Trp Leu Lys Thr	His 530	Met Asn Pro Arg	Ala 535	Val	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 ctacatccta ggccttctgg ggcttttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcacccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350
 tccaggtgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atccccgagcc aaagacagag tggcggtagc aggtggagtc tttttcatcc 500
 ttggaggcct cctgggattc attcctgttg cctggaatct tcatgggatc 550
 ctacgggact tctactcacc actggtgcct gacagcatga aatttgagat 600
 tggagaggct ctttacttgg gcattatttc ttccctgttc tccctgatag 650
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 gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
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 gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
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Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25				30	

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40				45	

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Ile	Thr	Gln	Cys	Asp	Ile	Tyr	Ser	Thr	Leu	Leu	Gly	Leu	Pro	Ala					
				65					70					75					
Asp	Ile	Gln	Ala	Ala	Gln	Ala	Met	Met	Val	Thr	Ser	Ser	Ala	Ile					
				80					85					90					
Ser	Ser	Leu	Ala	Cys	Ile	Ile	Ser	Val	Val	Gly	Met	Arg	Cys	Thr					
				95					100					105					
Val	Phe	Cys	Gln	Glu	Ser	Arg	Ala	Lys	Asp	Arg	Val	Ala	Val	Ala					
				110					115					120					
Gly	Gly	Val	Phe	Phe	Ile	Leu	Gly	Gly	Leu	Leu	Gly	Phe	Ile	Pro					
				125					130					135					
Val	Ala	Trp	Asn	Leu	His	Gly	Ile	Leu	Arg	Asp	Phe	Tyr	Ser	Pro					
				140					145					150					
Leu	Val	Pro	Asp	Ser	Met	Lys	Phe	Glu	Ile	Gly	Glu	Ala	Leu	Tyr					
				155					160					165					
Leu	Gly	Ile	Ile	Ser	Ser	Leu	Phe	Ser	Leu	Ile	Ala	Gly	Ile	Ile					
				170					175					180					
Leu	Cys	Phe	Ser	Cys	Ser	Ser	Gln	Arg	Asn	Arg	Ser	Asn	Tyr	Tyr					
				185					190					195					
Asp	Ala	Tyr	Gln	Ala	Gln	Pro	Leu	Ala	Thr	Arg	Ser	Ser	Pro	Arg					
				200					205					210					
Pro	Gly	Gln	Pro	Pro	Lys	Val	Lys	Ser	Glu	Phe	Asn	Ser	Tyr	Ser					
				215					220					225					
Leu	Thr	Gly	Tyr	Val															
				230															

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aagtcatcgc tcccgtggc tcagaacct ggctgtgcca gccggcaccc 150
 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cgccatcgtg tccctgagcg agaccgccca atgtggtccc cctgcacct 250
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaac 300
 gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggtttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150
 gtggggacaa gttctacgac cccctgcagc actggttgcta tgatgatgcc 200
 gtcgtgcctt tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300
 agaactgcga ctcagcccgg acctcggatg acaggctttg tcgcagtgtc 350
 agctaattgga acatcagggg aacgatgact cctggattct ccttcctggg 400
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
 gctgttttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550
 ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600
 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650
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 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750
 tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys	1	5	10	15
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser											110			

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttcctg gctgcgtccc taggtccggg ggcagccttc aaggctcgcca 250
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 gacgtggtac cgcagctcga ggggcgaggg gcagacctgc tcagagcgcc 400
 ggcccatccg caacctcagc ttccaggacc ttcacctgca ccatggaggc 450
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 gtgggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550
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 caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
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 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250
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 gggaaggtga gtggagaggg gcacctgccc cccgcccctcc ccatccccta 1900
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
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 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	1	5	10	15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	20	25	30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu				

	140		145		150
Ile Arg His His	His Ser Glu His Arg	Val His Gly Ala Met	Glu		
	155	160	165		
Leu Gln Val Gln	Thr Gly Lys Asp Ala	Pro Ser Asn Cys Val	Val		
	170	175	180		
Tyr Pro Ser Ser	Ser Gln Asp Ser Glu	Asn Ile Thr Ala Ala	Ala		
	185	190	195		
Leu Ala Thr Gly	Ala Cys Ile Val Gly	Ile Leu Cys Leu Pro	Leu		
	200	205	210		
Ile Leu Leu Leu	Val Tyr Lys Gln Arg	Gln Ala Ala Ser Asn	Arg		
	215	220	225		
Arg Ala Gln Glu	Leu Val Arg Met Asp	Ser Asn Ile Gln Gly	Ile		
	230	235	240		
Glu Asn Pro Gly	Phe Glu Ala Ser Pro	Pro Ala Gln Gly Ile	Pro		
	245	250	255		
Glu Ala Lys Val	Arg His Pro Leu Ser	Tyr Val Ala Gln Arg	Gln		
	260	265	270		
Pro Ser Glu Ser	Gly Arg His Leu Leu	Ser Glu Pro Ser Thr	Pro		
	275	280	285		
Leu Ser Pro Pro	Gly Pro Gly Asp Val	Phe Phe Pro Ser Leu	Asp		
	290	295	300		
Pro Val Pro Asp	Ser Pro Asn Phe Glu	Val Ile			
	305	310			

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttctgcc ctcctttcct gccaccgct gcttctggc 150
 ccttctccga ccccgctcta gcagcagacc tcctgggggc tgtgggttga 200
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgact 250
 ccgctcccg accagcgcc tgaccctggg gaaaggatgg ttcccgaggt 300
 gagggctctc tcctccttgc tgggactcgc gctgctctgg ttccccctgg 350
 actccacgc tcgagccgc ccagacatgt tctgcctttt ccatgggaag 400
 agatactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600
ggccccacca aagtcctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
ccccgaacca ggctgccag caccctccc actgccagac tcctgctgcc 800
aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgatgc 900
tgggagaaag agaggcccg gcacccagc cccactggc ctgagcgccc 950
ctctgagctt catcctcgc cacttcagac ccaagggagc aggcagcaca 1000
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
cgggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
tcggccccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
tgccagcgtg tgacctgtcc caccgagtac ccctgccgtc accccgagaa 1200
agtggctggg aagtgtgca agatttgccc agaggacaaa gcagaccctg 1250
gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
ctcgtccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350
cctggaacac gaggcctcgg acttggtgga gatctacctc tggaagctgg 1400
taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450
ccacacagcc agaatcttcc acttgactca gatcaagaa gtcaggaagc 1500
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550
gaaggtcact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgttattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	1	5	10	15
Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	20	25	30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	35	40	45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	50	55	60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	65	70	75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	80	85	90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	95	100	105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	110	115	120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	125	130	135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	140	145	150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	155	160	165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	170	175	180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	185	190	195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	200	205	210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	215	220	225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	230	235	240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	245	250	255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	260	265	270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	275	280	285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys				

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys Pro	
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser	Glu Ile Ser Ser Thr Arg	
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu	Val His Thr Ser Val Ser	
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe	Ala Leu Glu His Glu Ala	
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp Glu	
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro His	
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu Ala	
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp Pro	
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly Ala	
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr Lys	
440	445	450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
 ctgacctgcg ccaaggggta gtgagaccgc gcggcaacag cttgcggctg 50
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gctcctcggt atcgtgacct cgaggagcgc gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350
 ggcgccagcg ggaggtcacc gtgagaccgc acttgccctc gtgggcgccg 400
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
 gtgagctgcc gtccgggtgag cacgtttccc ccaaaccctg gactgactgc 550
 ttttaagggtcc gcaaggcggg ccaggggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggtgact gtacgttcct tctactctgg caccactctc 100
 cagggtgccca tggggcccag caccctctc ctcattctgt tccttttgtc 150
 atggtcggga cccctccaag gacagcagca ccaccttggt gagtacctgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
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gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
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gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
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ttcctcattc ttcaaagtgt ggccagttgt ggctcaaagc ctctatattt 1450
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ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
ttccctcctg ctctcctgcc ccatgtcaac aaatttcagg ctaaggatgc 1600
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
agcagtgttc ttcccctcag agtgacttgg ggaggagaa ataggaggag 1700
acgtccagct ctgtcctctc ttctcactc ctcccttcag tgtcctgagg 1750
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gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15

Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60

Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75

Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90

Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105

Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120

Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135

Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150

Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165

Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180

Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195

Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210

Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225

Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240

Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	260	265	270
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	275	280	285
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	290	295	300
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	305	310	315
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	320	325	330
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	335	340	345
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	350	355	360
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	365	370	375
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	380	385	390
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	395	400	405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 ccgctcagcg agagcctctc cgtggcttcc gcaccttgag cattaggcca 100
 gttctcctct tctctctaata ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttgggttctga gtctcctcaa gctgggatca gggcagtgga aggtgtttgg 250
 gccagacaag cctgtccagg ccttgggtgg ggaggacgca gcattctcct 300
 gtttctctgt tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
 tcgggctggt tccccggcc cacagcgaag tggaaaggct cacaaggaca 700
 ggatttgctc acagactcca ggacaaacag agacatgcat ggctgtttg 750
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 tccatgcggc atgtcatct gagccgagag gtggaatcca ggttacagat 850
 aggagatacc ttttctgagc ctatatcgtg gcacctggct accaaagtac 900
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
 tgactctgga tccagagacg gctcacccga agctctgcgt ttctgatctg 1100
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcaggga 1200
 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
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 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
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 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650
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 acattcttct ttagggatat taaggtctct ctcccagatc caaagtcccg 1750
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 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgttagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				

230										235					240				
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys					
				245					250					255					
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					
Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val					
				320					325					330					
Val	Ala	Ser	Gln	Ser	Phe	Gln	Ala	Gly	Lys	His	Tyr	Trp	Glu	Val					
				335					340					345					
Asp	Gly	Gly	His	Asn	Lys	Arg	Trp	Arg	Val	Gly	Val	Cys	Arg	Asp					
				350					355					360					
Asp	Val	Asp	Arg	Arg	Lys	Glu	Tyr	Val	Thr	Leu	Ser	Pro	Asp	His					
				365					370					375					
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Asn	Gly	Glu	His	Leu	Tyr	Phe	Thr					
				380					385					390					
Leu	Asn	Pro	Arg	Phe	Ile	Ser	Val	Phe	Pro	Arg	Thr	Pro	Pro	Thr					
				395					400					405					
Lys	Ile	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Cys	Gly	Thr	Ile	Ser	Phe					
				410					415					420					
Phe	Asn	Ile	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Thr	Cys	Arg					
				425					430					435					
Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Glu	Tyr	Pro	Ser	Tyr	Asn					
				440					445					450					
Glu	Gln	Asn	Gly	Thr	Pro	Ile	Val	Ile	Cys	Pro	Val	Thr	Gln	Glu					
				455					460					465					
Ser	Glu	Lys	Glu	Ala	Ser	Trp	Gln	Arg	Ala	Ser	Ala	Ile	Pro	Glu					
				470					475					480					
Thr	Ser	Asn	Ser	Glu	Ser	Ser	Ser	Gln	Ala	Thr	Thr	Pro	Phe	Leu					
				485					490					495					
Pro	Arg	Gly	Glu	Met															
				500															

<210> 149
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc aagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgcg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgggtggcggc ggggccgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
ggcgacggc tcccacggcc caggccccga ggaccgggcc ccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

caccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accacccttt cgacgaccac 550
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac cccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
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tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800
gaaacctgca aagagggtt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtcac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacia aggaggatga 1000
gggtcataga tttaaaaaat attttatata cttttattct cttactttat 1050
atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggt 1200
ttcaggcatg aaacctgcta ggaggtttag aaatgttctt atgtttatta 1250
atataccatt ggagtttgag gaaatttgtt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
ggtagcctaa tttatttaac tagtggttag tagactgggt ttactctatt 1400
taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
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acagtattaa ataataaaaa aaataatgac aggttatact cagtgttaacc 1650
tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
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ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctcacgcctg taatcctagc actttgggag gccaaggcgg gtggatcact 2050
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 agaggggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	1	5	10	15
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	20	25	30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	35	40	45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	50	55	60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	65	70	75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	80	85	90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	95	100	105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	110	115	120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	125	130	135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	140	145	150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	155	160	165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro				

	170	175	180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys	Asn
	185	190	195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln	Thr
	200	205	210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His	Cys
	215	220	225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly	Leu
	230	235	240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile	Pro
	245	250	255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tgggtggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
 tgcggcgagcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
 ttctggctttt ggtctcgggtg cccagggccc aggccgtgtg gttgggaaga 100
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtgccctc 150
 ccgggaaaag ggctttgcca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
 caccggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgccca tcatcttcac tcagctggag 400
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gagggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgcccaca 600
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 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159
 <211> 1665
 <212> DNA
 <213> Homo sapiens

<400> 159
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 gctgctgctg cccctgctct gggggaggga gagggcgga ggacagacaa 100
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150
 gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttaccc 200
 tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
 aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
 actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggtctctc 450
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600
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 gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
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 cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
 cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
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 cttctgcccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350
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 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450
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 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550
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 tcaaacctga atccacactg tgcctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
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Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
				20					25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50					55					60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65					70					75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80					85					90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95					100					105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

110										115					120				
Met	Glu	Lys	Gly	Ser	Ile	Lys	Trp	Asn	Tyr	Lys	His	His	Arg	Leu					
				125					130					135					
Ser	Val	Asn	Val	Thr	Ala	Leu	Thr	His	Arg	Pro	Asn	Ile	Leu	Ile					
				140					145					150					
Pro	Gly	Thr	Leu	Glu	Ser	Gly	Cys	Pro	Gln	Asn	Leu	Thr	Cys	Ser					
				155					160					165					
Val	Pro	Trp	Ala	Cys	Glu	Gln	Gly	Thr	Pro	Pro	Met	Ile	Ser	Trp					
				170					175					180					
Ile	Gly	Thr	Ser	Val	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Thr	Arg	Ser					
				185					190					195					
Ser	Val	Leu	Thr	Leu	Ile	Pro	Gln	Pro	Gln	Asp	His	Gly	Thr	Ser					
				200					205					210					
Leu	Thr	Cys	Gln	Val	Thr	Phe	Pro	Gly	Ala	Ser	Val	Thr	Thr	Asn					
				215					220					225					
Lys	Thr	Val	His	Leu	Asn	Val	Ser	Tyr	Pro	Pro	Gln	Asn	Leu	Thr					
				230					235					240					
Met	Thr	Val	Phe	Gln	Gly	Asp	Gly	Thr	Val	Ser	Thr	Val	Leu	Gly					
				245					250					255					
Asn	Gly	Ser	Ser	Leu	Ser	Leu	Pro	Glu	Gly	Gln	Ser	Leu	Arg	Leu					
				260					265					270					
Val	Cys	Ala	Val	Asp	Ala	Val	Asp	Ser	Asn	Pro	Pro	Ala	Arg	Leu					
				275					280					285					
Ser	Leu	Ser	Trp	Arg	Gly	Leu	Thr	Leu	Cys	Pro	Ser	Gln	Pro	Ser					
				290					295					300					
Asn	Pro	Gly	Val	Leu	Glu	Leu	Pro	Trp	Val	His	Leu	Arg	Asp	Ala					
				305					310					315					
Ala	Glu	Phe	Thr	Cys	Arg	Ala	Gln	Asn	Pro	Leu	Gly	Ser	Gln	Gln					
				320					325					330					
Val	Tyr	Leu	Asn	Val	Ser	Leu	Gln	Ser	Lys	Ala	Thr	Ser	Gly	Val					
				335					340					345					
Thr	Gln	Gly	Val	Val	Gly	Gly	Ala	Gly	Ala	Thr	Ala	Leu	Val	Phe					
				350					355					360					
Leu	Ser	Phe	Cys	Val	Ile	Phe	Val	Val	Val	Arg	Ser	Cys	Arg	Lys					
				365					370					375					
Lys	Ser	Ala	Arg	Pro	Ala	Ala	Gly	Val	Gly	Asp	Thr	Gly	Ile	Glu					
				380					385					390					
Asp	Ala	Asn	Ala	Val	Arg	Gly	Ser	Ala	Ser	Gln	Gly	Pro	Leu	Thr					
				395					400					405					

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420

Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 accctgttcc tgggtgtcac gtcggcctg gccgctgcc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttcggag gacaggagc ccaggaaggt gtccccagt 200
 aaggtgacag cctggggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagc caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacc tcagccatg acccttcct 650
 gctccacccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg					
			35						40					45					
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly					
			50						55					60					
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile					
			65						70					75					
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr					
			80						85					90					
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro					
			95						100					105					
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly					
			110						115					120					
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr					
			125						130					135					
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys					
			140						145					150					
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser					
			155						160					165					
Cys	Val	Pro	Glu	His															
			170																

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccttat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gcctagtgtt cggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50
 cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
 aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
 gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
 ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250
 cgacgtcat cgccccaga tggctcctga cagcagcca ctgcctcaag 300
 ccccgctaca tagttcacct ggggcagcac aacctcaga aggaggaggg 350
 ctgtgagcag acccggacag ccaactgagtc cttccccac cccggettca 400
 acaacagcct cccaacaaa gaccaccgca atgacatcat gctggtgaag 450
 atggcatcgc cagtctccat cacctgggt gtgcgacccc tcacctctc 500
 ctacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
 gcacgtccag ccccgagta cgctgcctc acaccttgcg atgcgccaac 600
 atcaccatca ttgagacca gaagtgtgag aacgcctacc ccggcaacat 650
 cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
 gccaggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750
 attatctcct ggggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
 ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
 acaattagac tggaccacc caccacagcc catcaccctc catttccact 900
 tgggtgtttg ttctgttca ctctgttaat aagaaacct aagccaagac 950
 cctctacgaa cattctttg gcctcctgga ctacaggaga tgctgtcact 1000
 taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050
 ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100
 tgtatcccca gcccaaaga cagctcctgg ccatatatca aggtttcaat 1150
 aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
 aaaa 1204

<210> 170
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 170
 Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
 1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	
				20					25					30	
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	
				35					40					45	
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	
				50					55					60	
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	
				65					70					75	
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	
				80					85					90	
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	
				95					100					105	
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	
				110					115					120	
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	
				125					130					135	
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	
				140					145					150	
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	
				155					160					165	
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	
				170					175					180	
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	
				185					190					195	
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	
				200					205					210	
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	
				215					220					225	
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	
				230					235					240	
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						
				245					250						

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
 ggctgcggga ctggaagtca tcggg 25

 <210> 172
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 172
 ctccaggcca tgaggattct gcag 24

 <210> 173
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 173
 cctctggtct gtaaccag 18

 <210> 174
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 174
 tctgtgatgt tgccggggta ggcg 24

 <210> 175
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 175
 cgtgtagaca ccaggctttc gggtg 25

 <210> 176
 <211> 18
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttgtt cttggtgttg ggcaagtcatt 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
 tgtgacacaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
 gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
 atttctactt ttttttttta gctattttact gtactttatg tataaaacia 750
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850
 ttgcaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
 1 5 10 15
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
 20 25 30
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
 35 40 45
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
 50 55 60
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
 65 70 75
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
 80 85 90
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
 95 100 105
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
 110 115 120
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
 125 130 135
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
 140 145 150

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

cctttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatcctgat atgacttgct acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaacaaa acttcctgtg ctaagtgcc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
 atactttctgg atctgggcag aaactattca cattcccctt ggagacatgt 200
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
 atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500
 ttcttgtttc atttcgagac tgccctctca gtgtttcctg ggatcccctc 550
 ccaaataaag tacttatatt ctc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cggtacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700
atgcctgccg ggggtattct gggggccccc tgggtgtgtg gggagtcctt 750
caaggtctgg tgcctgggg gtctgtggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttggtg gcctgggaac ttcttggaac tttactcct 1000
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

200	205	210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp		
215	220	225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp		
230	235	240
Ile Arg Met Ile Met Arg Asn Asn		
245		

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50
 ctcgctccctc gccgcgtccg cgaagcctgg agccggcgagg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgctc 150
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<210> 196
 <211> 150
 <212> PRT
 <213> Homo sapiens

<400> 196
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 20 25 30
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 35 40 45
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
 50 55 60
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
 65 70 75
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
 80 85 90
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
 95 100 105
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
 110 115 120
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
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 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
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<210> 197
 <211> 4842
 <212> DNA
 <213> Homo sapiens

<400> 197

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met	Ala	Pro	Gly	Trp	Ala	Gly	Val	Gly	Ala	Ala	Val	Arg	Ala	Arg	1	5	10	15
Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro	20	25	30	
Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val	35	40	45	
Asp	Cys	His	Gly	Leu	Gly	Leu	Arg	Ala	Val	Pro	Arg	Gly	Ile	Pro	50	55	60	
Arg	Asn	Ala	Glu	Arg	Leu	Asp	Leu	Asp	Arg	Asn	Asn	Ile	Thr	Arg	65	70	75	
Ile	Thr	Lys	Met	Asp	Phe	Ala	Gly	Leu	Lys	Asn	Leu	Arg	Val	Leu	80	85	90	
His	Leu	Glu	Asp	Asn	Gln	Val	Ser	Val	Ile	Glu	Arg	Gly	Ala	Phe	95	100	105	
Gln	Asp	Leu	Lys	Gln	Leu	Glu	Arg	Leu	Arg	Leu	Asn	Lys	Asn	Lys	110	115	120	
Leu	Gln	Val	Leu	Pro	Glu	Leu	Leu	Phe	Gln	Ser	Thr	Pro	Lys	Leu	125	130	135	
Thr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Gly	Ile	Pro	Arg	140	145	150	
Lys	Ala	Phe	Arg	Gly	Ile	Thr	Asp	Val	Lys	Asn	Leu	Gln	Leu	Asp	155	160	165	

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

455										460					465				
Ser	Pro	Arg	Arg	Leu	Ala	Asn	Lys	Arg	Ile	Ser	Gln	Ile	Lys	Ser					
				470					475					480					
Lys	Lys	Phe	Arg	Cys	Ser	Gly	Ser	Glu	Asp	Tyr	Arg	Ser	Arg	Phe					
				485					490					495					
Ser	Ser	Glu	Cys	Phe	Met	Asp	Leu	Val	Cys	Pro	Glu	Lys	Cys	Arg					
				500					505					510					
Cys	Glu	Gly	Thr	Ile	Val	Asp	Cys	Ser	Asn	Gln	Lys	Leu	Val	Arg					
				515					520					525					
Ile	Pro	Ser	His	Leu	Pro	Glu	Tyr	Val	Thr	Asp	Leu	Arg	Leu	Asn					
				530					535					540					
Asp	Asn	Glu	Val	Ser	Val	Leu	Glu	Ala	Thr	Gly	Ile	Phe	Lys	Lys					
				545					550					555					
Leu	Pro	Asn	Leu	Arg	Lys	Ile	Asn	Leu	Ser	Asn	Asn	Lys	Ile	Lys					
				560					565					570					
Glu	Val	Arg	Glu	Gly	Ala	Phe	Asp	Gly	Ala	Ala	Ser	Val	Gln	Glu					
				575					580					585					
Leu	Met	Leu	Thr	Gly	Asn	Gln	Leu	Glu	Thr	Val	His	Gly	Arg	Val					
				590					595					600					
Phe	Arg	Gly	Leu	Ser	Gly	Leu	Lys	Thr	Leu	Met	Leu	Arg	Ser	Asn					
				605					610					615					
Leu	Ile	Ser	Cys	Val	Ser	Asn	Asp	Thr	Phe	Ala	Gly	Leu	Ser	Ser					
				620					625					630					
Val	Arg	Leu	Leu	Ser	Leu	Tyr	Asp	Asn	Arg	Ile	Thr	Thr	Ile	Thr					
				635					640					645					
Pro	Gly	Ala	Phe	Thr	Thr	Leu	Val	Ser	Leu	Ser	Thr	Ile	Asn	Leu					
				650					655					660					
Leu	Ser	Asn	Pro	Phe	Asn	Cys	Asn	Cys	His	Leu	Ala	Trp	Leu	Gly					
				665					670					675					
Lys	Trp	Leu	Arg	Lys	Arg	Arg	Ile	Val	Ser	Gly	Asn	Pro	Arg	Cys					
				680					685					690					
Gln	Lys	Pro	Phe	Phe	Leu	Lys	Glu	Ile	Pro	Ile	Gln	Asp	Val	Ala					
				695					700					705					
Ile	Gln	Asp	Phe	Thr	Cys	Asp	Gly	Asn	Glu	Glu	Ser	Ser	Cys	Gln					
				710					715					720					
Leu	Ser	Pro	Arg	Cys	Pro	Glu	Gln	Cys	Thr	Cys	Met	Glu	Thr	Val					
				725					730					735					
Val	Arg	Cys	Ser	Asn	Lys	Gly	Leu	Arg	Ala	Leu	Pro	Arg	Gly	Met					
				740					745					750					

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu Thr	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu Ile	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr Phe	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn Arg	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser Leu	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro Glu	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu Gly	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser Glu	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys Ser	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro Thr	890	895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val Ala	905	910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly Thr	920	925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro Tyr	935	940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys Ile	950	955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp Ser	965	970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu Gly	980	985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp Cys	995	1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val Cys	1010	1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val Ile	1025	1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala Lys			

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Cys Ile Pro Leu Asp 1055	Lys Gly Phe Ser Cys 1060	Glu Cys Val Pro Gly 1065
Tyr Ser Gly Lys Leu 1070	Cys Glu Thr Asp Asn 1075	Asp Asp Cys Val Ala 1080
His Lys Cys Arg His 1085	Gly Ala Gln Cys Val 1090	Asp Thr Ile Asn Gly 1095
Tyr Thr Cys Thr Cys 1100	Pro Gln Gly Phe Ser 1105	Gly Pro Phe Cys Glu 1110
His Pro Pro Pro Met 1115	Val Leu Leu Gln Thr 1120	Ser Pro Cys Asp Gln 1125
Tyr Glu Cys Gln Asn 1130	Gly Ala Gln Cys Ile 1135	Val Val Gln Gln Glu 1140
Pro Thr Cys Arg Cys 1145	Pro Pro Gly Phe Ala 1150	Gly Pro Arg Cys Glu 1155
Lys Leu Ile Thr Val 1160	Asn Phe Val Gly Lys 1165	Asp Ser Tyr Val Glu 1170
Leu Ala Ser Ala Lys 1175	Val Arg Pro Gln Ala 1180	Asn Ile Ser Leu Gln 1185
Val Ala Thr Asp Lys 1190	Asp Asn Gly Ile Leu 1195	Leu Tyr Lys Gly Asp 1200
Asn Asp Pro Leu Ala 1205	Leu Glu Leu Tyr Gln 1210	Gly His Val Arg Leu 1215
Val Tyr Asp Ser Leu 1220	Ser Ser Pro Pro Thr 1225	Thr Val Tyr Ser Val 1230
Glu Thr Val Asn Asp 1235	Gly Gln Phe His Ser 1240	Val Glu Leu Val Thr 1245
Leu Asn Gln Thr Leu 1250	Asn Leu Val Val Asp 1255	Lys Gly Thr Pro Lys 1260
Ser Leu Gly Lys Leu 1265	Gln Lys Gln Pro Ala 1270	Val Gly Ile Asn Ser 1275
Pro Leu Tyr Leu Gly 1280	Gly Ile Pro Thr Ser 1285	Thr Gly Leu Ser Ala 1290
Leu Arg Gln Gly Thr 1295	Asp Arg Pro Leu Gly 1300	Gly Phe His Gly Cys 1305
Ile His Glu Val Arg 1310	Ile Asn Asn Glu Leu 1315	Gln Asp Phe Lys Ala 1320
Leu Pro Pro Gln Ser 1325	Leu Gly Val Ser Pro 1330	Gly Cys Lys Ser Cys 1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
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 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
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 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
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 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

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<210> 200
 <211> 24
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
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<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
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<222> 1-50
<223> Synthetic construct.

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<211> 753
<212> DNA
<213> Homo sapiens

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agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgccg ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtccgtt ttcctcccaa tattccttct caaacttggg 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr
 1 5 10 15
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
 20 25 30
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaaactgg caaaaatatt ctcgagggct ggccctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatcccaact gtccttgtgt tcggagccag gccacaccgt 50
cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatttt actgtcactt ccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
 gaggaataca ccacagggcat ggcagactgc atcttagtca acagccagtt 350
 cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400
 ctgatgtcct ctatccatct ctaaattgtca ccagctttga ctcaattgtt 450
 cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500
 ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
 ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600
 catctgatcg tggcaggtgg ttatgacgag agagtccctgg agaattgtga 650
 acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700
 atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctctc 750
 cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
 tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
 cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
 gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950
 accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000
 aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050
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 ttatggattg tagaccaggt tttgaaacca aaaaagaaac ctagaatcta 1150
 atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200
 ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250
 tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300
 tgtcattcca tgttcagcag agtattttta ttatatatttc tcgggattat 1350
 tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400
 atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450
 ataatgagag cagggctatt gtagttccca gattcaatcc accgaagtgt 1500
 tcaactgtcat ctgtaggga atttttgttt gtccctgtctt tgcctggatc 1550
 catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600
 actgagatat aataaaagggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	
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Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	
				20					25					30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	
				35					40					45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	
				50					55					60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	
				65					70					75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	
				80					85					90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	
				95					100					105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	
				110					115					120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	
				125					130					135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	
				140					145					150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	
				155					160					165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	
				170					175					180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	
				185					190					195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	
				200					205					210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	
				215					220					225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	
				230					235					240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	
				245					250					255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	
				260					265					270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
 275 280 285
 Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
 290 295 300
 Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
 305 310 315
 Arg Tyr Val Thr Lys Leu Leu Val
 320

<210> 211
 <211> 1554
 <212> DNA
 <213> Homo sapiens

<400> 211
 gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50
 cttcgcgac ttcgccgtta ccttcttgct ggcgttggtg ggagccgtgc 100
 tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
 ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtgaag 200
 tttgcatgag ttcttggtta atttgcatga gagatatggg cctgtggtct 250
 ccttctggtt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300
 ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaacat 350
 gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400
 accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
 agtaactttg cctcctcct aaagctttca gaagaattat tagataaatg 500
 gctctctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
 gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
 gatgatcagg aagtcattcg cttccagaag aatcatggca cagtttggtc 650
 tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700
 ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
 aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
 tgactcctta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
 gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
 tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950
 tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tggtcgaact 1050
 gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggtagttca ggatcctaata acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
 ctcaggcaca caggagtgtc cagagttgag gtttgcatat atggtgacca 1300
 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
 ggacagggtta ttgaaacaaa gtatgaactg gtaacatcat caagggaaga 1400
 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttataaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu	1	5	10	15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala	20	25	30	
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu	35	40	45	
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	50	55	60	
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	65	70	75	
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	80	85	90	
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	95	100	105	
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	110	115	120	
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	125	130	135	
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu				

140										145					150				
Asp	Lys	Trp	Leu	Ser	Tyr	Pro	Glu	Thr	Gln	His	Val	Pro	Leu	Ser					
				155					160					165					
Gln	His	Met	Leu	Gly	Phe	Ala	Met	Lys	Ser	Val	Thr	Gln	Met	Val					
				170					175					180					
Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	Glu	Val	Ile	Arg	Phe	Gln					
				185					190					195					
Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	Gly	Lys	Gly	Phe	Leu					
				200					205					210					
Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	Lys	Gln	Tyr	Glu					
				215					220					225					
Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	Ile	Ile	Lys					
				230					235					240					
Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	Asp	Ser					
				245					250					255					
Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	Ser					
				260					265					270					
Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys					
				275					280					285					
Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys					
				290					295					300					
Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val					
				305					310					315					
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu					
				320					325					330					
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln					
				335					340					345					
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg					
				350					355					360					
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro					
				365					370					375					
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp					
				380					385					390					
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly					
				395					400					405					
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr					
				410					415					420					
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val					
				425					430					435					

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100
 tcagggttg tgccctctcg ctctctgacg ctcttgccgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaaata 700
 tgttttgtag taacattaag acttatatac agtttttagg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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 cctgggctct cccagcctc cttcgactcg gagcggtca ggagacagaa 100
 gaccgggctt gctgcagccc catagtgtccc cggaacgagt ggaaggccct 150
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450
 ccaggccatc cgggcagccc agggctctact ggctgcggt gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccgga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgtcc ccctgaggcc ctgctgatcc gcacccatt cctcccctcc 650
 catggcaaaa aaccccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	
1				5					10					15	
Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	
			20						25					30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	
				35					40					45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	
				50					55					60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	
				65					70					75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	
				80					85					90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	
				95					100					105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	
				110					115					120	
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr	
				125					130					135	
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly	
				140					145					150	
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr	
				155					160					165	
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly	
				170					175					180	
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser	
				185					190					195	

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100
tctatctggt catctgtggc caggatgatg gtcctcccggt ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgga 200

gcggggccac atctcaccta agtccccccc catggccaat tccactctcc 250
 tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggtggt ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cacgaccag ccaagatctg 650
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 tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggtg 750
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 gttgggcctc aggcaggag gggggtggag acgaggagat gccaagtggg 950
 gccagggcca agtctcaagt ggcagagaaa gggccccag tgctggtccc 1000
 aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050
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 ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
 gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
 gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
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<210> 218
<211> 252
<212> PRT
<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130 "	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219
 <211> 2065
 <212> DNA
 <213> Homo sapiens

<400> 219
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 agctcgaggg gagactttga cttcaagcca cagaattggt ggaagtgtgc 200
 gcgccgcgcgc cgccgtcgct cctgcagcgc tgtcgacctg gccgctagca 250
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 ggctgcccgt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450
 aagtgtctgg tgggtgtgca ctgcaaccgc gccacggact ccaagggtc 500
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 ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
 aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650
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 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaaa 1950
 ttcaaataat ccataatctaa atttagtgca atatcttgct ttttgtatag 2000
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 tatatgttaa aaaaa 2065

<210> 220
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 220
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 1 5 10 15
 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
 20 25 30
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
 35 40 45
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
 50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
 65 70 75
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
 140 145 150
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
 170 175 180
 Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
 185 190 195
 Phe Leu Val Phe Pro Leu
 200

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttggag tccg 24

<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
cgtgctggag ggcaagtgtc tggagggtgtg cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
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ta 902

<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
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Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30
Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met	Phe	Ala	Leu	Gly	Leu	Pro	Phe	Leu	Val	Leu	Leu	Val	Ala	Ser
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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly	
350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	620	625	630
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	635	640	645
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	650	655	660
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	665	670	675
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	680	685	690
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	695	700	705
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	710	715	720
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	725	730	735
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	740	745	750
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	755	760	765
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	770	775	780
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	785	790	795
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	800	805	810
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	815	820	825
Arg	Asp	Lys	Ile	Tyr	Val	Phe									830		

<210> 228
 <211> 2848
 <212> DNA
 <213> Homo sapiens

<400> 228
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 ttgggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150
 gctttgtgtc tccgtcccc aggctctccc caaggcccag cctgcagagc 200

tgtctgtgga agttccagaa aactatggtg gaaatttccc tttatacctg 250
 accaagttgc cgctgccccg tgagggggct gaaggccaga tctgtctgtc 300
 aggggactca ggcaaggcaa ctgagggccc atttgctatg gatccagatt 350
 ctggcttccct gctggtgacc agggccctgg accgagagga gcaggcagag 400
 taccagctac aggtcaccct ggagatgcag gatggacatg tcttgtgggg 450
 tccacagcct gtgcttgtgc acgtgaagga tgagaatgac caggtgcccc 500
 atttctctca agccatctac agagctcggc tgagccgggg taccaggcct 550
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 tgggtgatga tgagaatgac aacgtgccta tctgcctcc cctgacccc 1150
 acagtcagca tccctgagct cagtccacca ggtactgaag tgactagact 1200
 gtcagcagag gatgcagatg cccccggctc cccaattcc cacgttgtgt 1250
 atcagctcct gagccctgag cctgaggatg gggtagagg gagagccttc 1300
 caggtggacc ccacttcagg cagtgtgacg ctgggggtgc tcccactccg 1350
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 cagaggggtg cttcagcagc acgtgtgaag tcgaagtcgc agtcacagat 1450
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

Met	Val	Pro	Ala	Trp	Leu	Trp	Leu	Leu	Cys	Val	Ser	Val	Pro	Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

20										25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	320	325	330
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	335	340	345
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	350	355	360
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	365	370	375
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	380	385	390
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	395	400	405
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	410	415	420
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	425	430	435
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	440	445	450
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	455	460	465
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	470	475	480
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	485	490	495
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	500	505	510
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	515	520	525
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	530	535	540
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	545	550	555
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	560	565	570
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	575	580	585
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	590	595	600
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly			

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp 620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu 635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His 650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser 665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val 680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr 695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile 710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val 725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg 740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val 755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile 770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp 785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val 800	805	

<210> 230
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 230
 cgcccttaccg cgcagcccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttctgg aaatctccct cctccttcaa tgggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaa at ccttcctgag 250
atcccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggaggggtga 450
agattggaca ttcgtttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
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ggaaaggag ccagcgacaa cccttgctcc gaagtgtacc atggaccca 850

cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234
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 20 25 30
 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165

Gly Lys Gly Val	Arg Arg Pro Ala Val	Trp Leu Asn Ala Gly Ile
170		175 180
His Ser Arg Glu	Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala	
185		190 195
Arg Lys Ile Val	Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser	
200		205 210
Ile Leu Glu Lys	Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro	
215		220 225
Asp Gly Tyr Val	Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys	
230		235 240
Thr Arg Ser Arg	Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro	
245		250 255
Asn Arg Asn Trp	Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp	
260		265 270
Asn Pro Cys Ser	Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	
275		280 285
Val Glu Val Lys	Ser Val Val Asp Phe Ile Gln Lys His Gly Asn	
290		295 300
Phe Lys Gly Phe	Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met	
305		310 315
Tyr Pro Tyr Gly	Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu	
320		325 330
Leu Asp Lys Val	Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val	
335		340 345
Ser Gly Thr Glu	Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr	
350		355 360
Pro Ala Ser Gly	Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile	
365		370 375
Lys Phe Ala Phe	Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly	
380		385 390
Phe Leu Leu Pro	Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr	
395		400 405
Trp Leu Gly Leu	Lys Thr Ile Met Glu His Val Arg Asp Asn Leu	
410		415 420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235

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cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
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agatgggaag tgccctcttc gtcaagaagg agctgcagct gcaggcaa 500
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aactggaaca ggccttgtca gccagaacac tgataaagtg gagccactca 950
ctccagaaaa ggtggataga ggtgttcac cccagatttt ccatttctgc 1000
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tgcacaagaa ataacaaacc acatccctct ttctgttctg aggtgcatt 1400
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aatcaccaaa ccatcaacag ggacccagc cacaagccaa cacccattaa 1500
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 aaatacgcca acccaggtta ggcacctcta ttgcagaatt acaataacac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys	
1				5					10					15	
Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr	
				20					25					30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr	
				35					40					45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val	
				50					55					60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val	
				65					70					75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr	
				80					85					90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr	
				95					100					105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser	
				110					115					120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala	
				125					130					135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly	
				140					145					150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe	
				155					160					165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys	
				170					175					180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp	
				185					190					195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala	

	200		205		210
Lys Trp Glu Lys	Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe			
	215	220			225
Pro Phe Leu Val	Gly Glu Gln Val Thr	Val Gln Val Pro Met Met			
	230	235			240
His Gln Lys Glu	Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn			
	245	250			255
Cys Phe Val Leu	Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe			
	260	265			270
Phe Val Leu Pro	Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala			
	275	280			285
Leu Ser Ala Arg	Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys			
	290	295			300
Arg Trp Ile Glu	Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser			
	305	310			315
Tyr Asn Leu Glu	Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala			
	320	325			330
Phe Asp Lys Asn	Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser			
	335	340			345
Leu Gln Val Ser	Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser			
	350	355			360
Glu Glu Gly Thr	Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile			
	365	370			375
Val Arg Ser Lys	Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn			
	380	385			390
Arg Thr Phe Leu	Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile			
	395	400			405
Leu Phe Leu Gly	Lys Val Glu Asn Pro	Thr Lys Ser			
	410	415			

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctggtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaaac ccaggcatcc 50

agctgcccac ggcctgagtcc aagattcttc ccaggaacac aaacgtagga 100
 gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150
 ctttctcaag aatcctctgt tctttgccct cttaaagtctt ggtacatcta 200
 ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250
 aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
 agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
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 ggccagcact gccaccaact ctgagtccag cacaacctcc agtggggcca 950
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 gccaccaact ctgagtccag cagcactcc agtggggcca gcacagccac 1050
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 ctgagtccag cagcactcc agtggggcca gcacagccac caactctgag 1150
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 gcaactgccac caactctgag tccagcacia cctccagtgg ggtcagcaca 1450
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 agatgagcgg gaggaacagc gggccctgag cagccccgga agcaagtgcc 2050
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 cattcatccc aggagacccc tccagcttt gtttgagatc ctgaaaatct 2150
 tgaagaaggt attcctcacc tttcttgcc ttaccagaca ctggaaagag 2200
 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300
 gatgaactca gttataggag aaaacctcca tgctggactc catctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
 1 5 10 15
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	80	85	90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	95	100	105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala			

365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr	Ala
380	385	390
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr	Ala
395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr	Ala
410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr	Ala
425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr	Val
440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr	Ala
455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr	Ala
470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser	His Ser Ala Ser Thr	Ala
485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu	Ile
500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val	Ala Ala Val Gly Leu	Phe
515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg	Asn
530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro	His Gly Leu Asn His	Gly
545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His	Gly Ala Pro His Arg	Pro
560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser	Ile
575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser	Gly Pro	
590	595	

<210> 244
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggacccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgaacct tcccagcaat atgcatcttg cacgtctggt cggctcctgc 100

tccctccttc tgctactggg ggccctgtct g gatgggcgg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgaggggtg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tggggtcaac aacgtgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgccc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700
 tccagccatc aaggaggggc cacaaccacg ccgtttagcct ctggggcctc 750
 agtcaacacg cctttcatca accttcccg cctgtggagg agcgtcgcca 800
 acatcatgcc ctaaactggc atccggcctt gctggggagaa taatgtcgcc 850
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 tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu	1	5	10	15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	

Gly	Lys	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
				185					190					195
Lys	Glu	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
			200						205					210
Ser	Ser	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
			215						220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp	Arg
			230						235					240
Ser	Val	Ala	Asn	Ile	Met	Pro								
			245											

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcat cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctct gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccatt gagaaggatca ttgaaggat caaccgagg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252

ctccgggtcc ccaggggctg cgccggggccg gcctggcaag ggggacgagt 50
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tgaccctgac tcaactccagg tccggaggcg ggggcccccg gggcgactcg 150
ggggcggaacc gggggcgga gctgccgcc gtgagtccgg ccgagccacc 200
tgagcccgag ccgcgggaca ccgtcgctcc tgctctccga atgctgcgca 250
ccgcgatggg cctgaggagc tggctcgccg ccccatgggg cgcgctgccg 300
cctcgccac cgctgctgct gctcctgctg ctgctgctcc tgctgcagcc 350
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acagcccttc tgctgagcag ggatggcagg accctgtacg tgggtgctcg 500
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cccgggaaag gaagatcaac tcacccctgc agctcccaga ccgcgtgctg 1500
 aacttctca aggaccactt cctgatggac gggcaggacc gaagccgcat 1550
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 tccctggcct gcaccacacc tacgatgtcc tcttctggg cactggtgac 1650
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 gcctctacca gcctcagctg gccaccaggc cgtggatcca ggacatcgag 1950
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 <211> 837
 <212> PRT
 <213> Homo sapiens

<400> 253
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 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

80										85					90				
Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr					
				95					100					105					
Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys					
				110					115					120					
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile					
				125					130					135					
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly					
				140					145					150					
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn					
				155					160					165					
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp					
				170					175					180					
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala					
				185					190					195					
Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe					
				200					205					210					
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro					
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Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe					
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Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu					
				260					265					270					
Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile					
				275					280					285					
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp					
				290					295					300					
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp					
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Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro					
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Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr					
				335					340					345					
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val					
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Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys					
				365					370					375					

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380		385	390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395		400	405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
410		415	420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
425		430	435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
440		445	450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
455		460	465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
470		475	480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
485		490	495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
500		505	510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
515		520	525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
530		535	540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
545		550	555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
560		565	570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
575		580	585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
590		595	600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
605		610	615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
620		625	630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
635		640	645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
650		655	660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val

	665		670		675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro		
	680	685	690		
Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys		
	695	700	705		
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val		
	710	715	720		
Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe		
	725	730	735		
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln		
	740	745	750		
Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu		
	755	760	765		
Pro Pro Glu Thr	Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr		
	770	775	780		
Pro Leu Asp His	Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro		
	785	790	795		
Gly Ala Arg Val	Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile		
	800	805	810		
Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg		
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Val Arg Leu Gly	Ser Glu Ile Arg Asp	Ser Val Val			
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 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 254
 agcccgtagca gaatctgctc ctgg 24

<210> 255
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 255
 tgaagccagg gcagcgtcct ctgg 24

<210> 256
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 <212> DNA
 <213> Artificial

<220>
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<400> 256
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<210> 257
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 <212> DNA
 <213> Artificial

<220>
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<400> 257
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<210> 258
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 258
 gagctgcaga tcttctcatc gggacagccc gtgcagaatc tgctc 45

<210> 259
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 3635
 <223> unknown base

<400> 259
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<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
230 235 240

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530										535					540				
Ser	Gly	Arg	Phe	Asp	Met	Phe	Val	Arg	Phe	Met	Gly	Asn	Phe	Glu					
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Lys	Thr	Cys	Leu	Ile	Pro	Asn	Gln	Asn	Val	Lys	Leu	Val	Val	Leu					
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Leu	Phe	Asn	Ser	Asp	Ser	Asn	Pro	Asp	Lys	Ala	Lys	Gln	Val	Glu					
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Leu	Met	Arg	Asp	Tyr	Arg	Ile	Lys	Tyr	Pro	Lys	Ala	Asp	Met	Gln					
				590					595					600					
Ile	Leu	Pro	Val	Ser	Gly	Glu	Phe	Ser	Arg	Ala	Leu	Ala	Leu	Glu					
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Val	Gly	Ser	Ser	Gln	Phe	Asn	Asn	Glu	Ser	Leu	Leu	Phe	Phe	Cys					
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Asp	Val	Asp	Leu	Val	Phe	Thr	Thr	Glu	Phe	Leu	Gln	Arg	Cys	Arg					
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Ser	Gln	Tyr	Asp	Pro	Lys	Ile	Val	Tyr	Ser	Gly	Lys	Val	Pro	Ser					
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Asp	Asn	His	Phe	Ala	Phe	Thr	Gln	Lys	Thr	Gly	Phe	Trp	Arg	Asn					
				680					685					690					
Tyr	Gly	Phe	Gly	Ile	Thr	Cys	Ile	Tyr	Lys	Gly	Asp	Leu	Val	Arg					
				695					700					705					
Val	Gly	Gly	Phe	Asp	Val	Ser	Ile	Gln	Gly	Trp	Gly	Leu	Glu	Asp					
				710					715					720					
Val	Asp	Leu	Phe	Asn	Lys	Val	Val	Gln	Ala	Gly	Leu	Lys	Thr	Phe					
				725					730					735					
Arg	Ser	Gln	Glu	Val	Gly	Val	Val	His	Val	His	His	Pro	Val	Phe					
				740					745					750					
Cys	Asp	Pro	Asn	Leu	Asp	Pro	Lys	Gln	Tyr	Lys	Met	Cys	Leu	Gly					
				755					760					765					
Ser	Lys	Ala	Ser	Thr	Tyr	Gly	Ser	Thr	Gln	Gln	Leu	Ala	Glu	Met					
				770					775					780					
Trp	Leu	Glu	Lys	Asn	Asp	Pro	Ser	Tyr	Ser	Lys	Ser	Ser	Asn	Asn					
				785					790					795					
Asn	Gly	Ser	Val	Arg	Thr	Ala													
				800															

<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50
tgacaccttc cctttcggcc ttgaggttcc cagcctggtg gccccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttg ctatggcett cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccaccattc 500
 tggtcgatca aaccaaaciaa tgtttccatt gttttgcatg cagaggaacc 550
 ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
 aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
 ccatatgtta cctcatacaa gtcacctgtc accactttag ataagagcac 700
 tggcattgag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750
 aaactgcatg agaaaaaccc gaagagtttg gaaagcaccg agagagttgg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850
 acaggcactt cttagtgaac ccagcaaccc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
 tagatcaagg agagtcacag cttattaaa agtttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga ttttaagcaa 1250
 ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300
 ataaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350
 atgtgttatg aacaattttc atatgcacta aaaaccta ataaaaataa 1400
 attttggttc aggaaaaaa 1419

<210> 265
 <211> 350
 <212> PRT
 <213> Homo sapiens

<400> 265
 Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser
 1 5 10 15
 Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu
 20 25 30
 Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
 35 40 45
 Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50										55					60				
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys					
				65					70					75					
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu					
				80					85					90					
Thr	Asn	Pro	Ile	Ser	Glu	Glu	Thr	Thr	Thr	Phe	Pro	Thr	Gly	Gly					
				95					100					105					
Phe	Thr	Pro	Glu	Ile	Gly	Lys	Lys	Lys	His	Thr	Glu	Ser	Thr	Pro					
				110					115					120					
Phe	Trp	Ser	Ile	Lys	Pro	Asn	Asn	Val	Ser	Ile	Val	Leu	His	Ala					
				125					130					135					
Glu	Glu	Pro	Tyr	Ile	Glu	Asn	Glu	Glu	Pro	Glu	Pro	Glu	Pro	Glu					
				140					145					150					
Pro	Ala	Ala	Lys	Gln	Thr	Glu	Ala	Pro	Arg	Met	Leu	Pro	Val	Val					
				155					160					165					
Thr	Glu	Ser	Ser	Thr	Ser	Pro	Tyr	Val	Thr	Ser	Tyr	Lys	Ser	Pro					
				170					175					180					
Val	Thr	Thr	Leu	Asp	Lys	Ser	Thr	Gly	Ile	Glu	Ile	Ser	Thr	Glu					
				185					190					195					
Ser	Glu	Asp	Val	Pro	Gln	Leu	Ser	Gly	Glu	Thr	Ala	Ile	Glu	Lys					
				200					205					210					
Pro	Glu	Glu	Phe	Gly	Lys	His	Pro	Glu	Ser	Trp	Asn	Asn	Asp	Asp					
				215					220					225					
Ile	Leu	Lys	Lys	Ile	Leu	Asp	Ile	Asn	Ser	Gln	Val	Gln	Gln	Ala					
				230					235					240					
Leu	Leu	Ser	Asp	Thr	Ser	Asn	Pro	Ala	Tyr	Arg	Glu	Asp	Ile	Glu					
				245					250					255					
Ala	Ser	Lys	Asp	His	Leu	Lys	Arg	Ser	Leu	Ala	Leu	Ala	Ala	Ala					
				260					265					270					
Ala	Glu	His	Lys	Leu	Lys	Thr	Met	Tyr	Lys	Ser	Gln	Leu	Leu	Pro					
				275					280					285					
Val	Gly	Arg	Thr	Ser	Asn	Lys	Ile	Asp	Asp	Ile	Glu	Thr	Val	Ile					
				290					295					300					
Asn	Met	Leu	Cys	Asn	Ser	Arg	Ser	Lys	Leu	Tyr	Glu	Tyr	Leu	Asp					
				305					310					315					
Ile	Lys	Cys	Val	Pro	Pro	Glu	Met	Arg	Glu	Lys	Ala	Ala	Thr	Val					
				320					325					330					
Phe	Asn	Thr	Leu	Lys	Asn	Met	Cys	Arg	Ser	Arg	Arg	Val	Thr	Ala					
				335					340					345					

Leu Leu Lys Val Tyr
350

<210> 266
<211> 2403
<212> DNA
<213> Homo sapiens

<400> 266
cggctcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50
acagctggcc tgacctcaa atcatccatc caccctgct gtcactgtt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctggtgtc aggacagtgg caagtcaactg 200
gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tggccacct ctacagagat ggggaagact 350
gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400
gactccattg caggggggcg tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggctgtatg ggtgctggtt cagttcccag atttacgatg 500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttctctc 550
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600
ctcaggctgg tccccccagc ccacagccaa gtggaaagggt ccacaaggac 650
aggatttgct ttcagactcc agagcaaagt cagatgggta cagcctgtat 700
gatgtggaga tctccattat agtcaggaa aatgctggga gcatattgtg 750
ttccatccac cttgctgagc agagtcatga ggtggaatcc aaggatttga 800
taggagagac gtttttccag ccctcacctt ggcgcctggc ttctatttta 850
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgttttcttc aaatccaaag ggaaaatcca ggcggaactg gactggagaa 950
gaaagcacgg acaggcagaa ttgagagacg cccggaaca cgcagtggag 1000
gtgactctgg atccagagac ggctcaccg aagctctgcg tttctgatct 1050
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

ccaacaatgg gtattgggtc ctgagactga caacagaaca tttgtatttc 1300
 acattcaatc cccattttat cagcctcccc cccagcacc ctcctacacg 1350
 agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata 1400
 caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
 ttgttgagac cctatatcca gcatgcatg tatgacgagg aaaaggggac 1500
 tcccatattc atatgtccag tgcctgggg atgagacaga gaagaccctg 1550
 cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600
 ccgacaggtg gccccagctt cctctccgga gcctgcatc agagagtcac 1650
 gccccccact ctcctttagg gagctgaggt tcttctgccc tgagccctgc 1700
 agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750
 gggagtcaga agccatggct gccctgaagt ggggacggaa tagactcaca 1800
 ttaggttttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
 cacaacctcc caggctctc atttgctagt cacggacagt gattcctgcc 1900
 tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950
 tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000
 accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050
 aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100
 ataaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
 gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
 gtccatatcc ctcatataca cagacacaaa aattctaaat aaaattttta 2250
 caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
 ggtttgtccc acaaatgcag agttgggtta atatttaaat atcaaccagt 2350
 gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
 aaa 2403

<210> 267
 <211> 466
 <212> PRT
 <213> Homo sapiens

<400> 267
 Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
 1 5 10 15
 Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20										25					30				
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu					
				35					40					45					
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe					
				50					55					60					
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser					
				65					70					75					
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp					
				80					85					90					
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr					
				95					100					105					
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile					
				110					115					120					
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly					
				125					130					135					
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile					
				140					145					150					
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala					
				155					160					165					
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg					
				170					175					180					
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile					
				185					190					195					
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu					
				200					205					210					
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu					
				215					220					225					
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu					
				230					235					240					
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile					
				245					250					255					
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp					
				260					265					270					
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys					
				275					280					285					
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys					
				290					295					300					
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro					
				305					310					315					

Gln	Glu	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val	320	325	330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val	335	340	345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp	350	355	360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn	365	370	375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr	380	385	390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr	395	400	405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe	410	415	420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys	425	430	435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr	440	445	450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp	455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
 ccttcacagg actcttcatt gctggttggc aatgatgtat cggccagatg 50
 tgggtgagggc taggaaaaga gtttggttggg aaccctgggt tatcggcctc 100
 gtcacatcca tatccctgat tgccttgcca gtgtgcattg gactcactgt 150
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
 tgttttacat gaaaagctgc aagatgctgt aggacccctt aaagtagatc 500

ctcaactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
 ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
 caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650
 ctagcctgca gtgggatggg agtcacgcgt gtggagcaac ctttaattaat 700
 gccacatggc ttgtgagtgc tgctcactgt tttaacaacat ataagaaccc 750
 tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
 aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
 catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
 aaatgcagta catagagttt gtctccctga tgcacccat gagtttcaac 950
 caggatgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000
 tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
 aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
 tatgtgctgg ctccctagaa ggaaaaacag atgcatgcca gggatgactct 1150
 ggaggaccac tgggttagttc agatgctaga gatattctgg accttgctgg 1200
 aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt 1250
 atactagagt tacggccttg cgggactgga ttacttcaaa aactggatatc 1300
 taagagacaa aagcctcatg gaacagataa catttttttt tggttttttg 1350
 gtgtggaggc cattttttaga gatacagaat tggagaagac ttgcaaaaca 1400
 gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450
 ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc 1500
 tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550
 atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600
 cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650
 agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
 attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750
 tcccctacat ttatttgga cagaaaagta ttaggtgttt ttcttagtgg 1800
 aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900
 tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000
 caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
 cca 2103

<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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 catgctgggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
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<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
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35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

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<210> 273
 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273

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Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu	35	40	45	
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe	50	55	60	
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile	65	70	75	
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu	80	85	90	
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys	95	100	105	
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met	110	115	120	
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser				

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Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274
 <211> 2063
 <212> DNA
 <213> Homo sapiens

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caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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				20					25					30
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
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Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
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Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255

Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala	Lys
260	265		270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn	Asp
275	280		285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly	Thr
290	295		300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr	Pro
305	310		315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln	Asn
320	325		330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln	Val
335	340		345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly	Glu
350	355		360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly	Val
365	370		375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln	Ser
380	385		390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly	Cys
395	400		405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala	Tyr
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425	430		

<210> 276

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 276

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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

290										295					300				
Phe	Asn	Val	Ile	Arg	His	Ala	Val	Leu	Leu	Pro	Ala	Asp	Ser	Pro					
				305					310					315					
Thr	Ala	Pro	His	Ile	Tyr	Ala	Val	Phe	Thr	Ser	Gln	Trp	Gln	Val					
				320					325					330					
Gly	Gly	Thr	Arg	Ser	Ser	Ala	Val	Cys	Ala	Phe	Ser	Leu	Leu	Asp					
				335					340					345					
Ile	Glu	Arg	Val	Phe	Lys	Gly	Lys	Tyr	Lys	Glu	Leu	Asn	Lys	Glu					
				350					355					360					
Thr	Ser	Arg	Trp	Thr	Thr	Tyr	Arg	Gly	Pro	Glu	Thr	Asn	Pro	Arg					
				365					370					375					
Pro	Gly	Ser	Cys	Ser	Val	Gly	Pro	Ser	Ser	Asp	Lys	Ala	Leu	Thr					
				380					385					390					
Phe	Met	Lys	Asp	His	Phe	Leu	Met	Asp	Glu	Gln	Val	Val	Gly	Thr					
				395					400					405					
Pro	Leu	Leu	Val	Lys	Ser	Gly	Val	Glu	Tyr	Thr	Arg	Leu	Ala	Val					
				410					415					420					
Glu	Thr	Ala	Gln	Gly	Leu	Asp	Gly	His	Ser	His	Leu	Val	Met	Tyr					
				425					430					435					
Leu	Gly	Thr	Thr	Thr	Gly	Ser	Leu	His	Lys	Ala	Val	Val	Ser	Gly					
				440					445					450					
Asp	Ser	Ser	Ala	His	Leu	Val	Glu	Glu	Ile	Gln	Leu	Phe	Pro	Asp					
				455					460					465					
Pro	Glu	Pro	Val	Arg	Asn	Leu	Gln	Leu	Ala	Pro	Thr	Gln	Gly	Ala					
				470					475					480					
Val	Phe	Val	Gly	Phe	Ser	Gly	Gly	Val	Trp	Arg	Val	Pro	Arg	Ala					
				485					490					495					
Asn	Cys	Ser	Val	Tyr	Glu	Ser	Cys	Val	Asp	Cys	Val	Leu	Ala	Arg					
				500					505					510					
Asp	Pro	His	Cys	Ala	Trp	Asp	Pro	Glu	Ser	Arg	Thr	Cys	Cys	Leu					
				515					520					525					
Leu	Ser	Ala	Pro	Asn	Leu	Asn	Ser	Trp	Lys	Gln	Asp	Met	Glu	Arg					
				530					535					540					
Gly	Asn	Pro	Glu	Trp	Ala	Cys	Ala	Ser	Gly	Pro	Met	Ser	Arg	Ser					
				545					550					555					
Leu	Arg	Pro	Gln	Ser	Arg	Pro	Gln	Ile	Ile	Lys	Glu	Val	Leu	Ala					
				560					565					570					
Val	Pro	Asn	Ser	Ile	Leu	Glu	Leu	Pro	Cys	Pro	His	Leu	Ser	Ala					
				575					580					585					

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 278
 ctgctggtga aatctggcgt ggag 24

<210> 279
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgta tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
agggtccctt agccgggagc agggcgcgca gccaggctg agatccgcgg 50
cttccgtaga agtgagcatg gctgggcagc gagtgcttct tctagtgggc 100
ttccttctcc ctggggctct gctctcagag gctgccaaaa tcctgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacggtcac aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaagagaa cttcgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcctgattg ctgagaagct tgggaagcca 550
tttgtggcca ttctttccac ttcattcggc tctttggaat ttgggctacc 600
aatcccttg tttatgttc cagtattccg ttccttgctg actgatcaca 650
tggaacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
tttcacagaa ggctctaggc cagttttgtc tcactttcta ctgaaagcag 800
agttgtgggtt cattaactct gactttgcct ttgattttgc tcgacctctg 850
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctgggt 950
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100
 atgtgaaaat tgtggactgg cttcctcaga gtgacctcct ggctcaccca 1150
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200
 catccagcat ggtgtgcccc tgggtggggat ccctctcttt ggagaccagc 1250
 ctgaaaacat ggtccgagta gaagccaaaa agtttgggtgt ttctattcag 1300
 ttaaagaagc tcaaggcaga gacattggct ctttaagatga aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcacctgc 1400
 gctcccaccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
 gtcctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500
 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550
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 ttccagtctt cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900
 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950
 aaaatccacc ttccttctca tgcgcctctc cgaatcacac cctgactctt 2000
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150
 tgtgcttgag agttcagggc cggacacagg ctcacaggtc tccacattgg 2200
 gtccctgtct ctgggtgcca cagtgaagct cttcttggct gagcaggcat 2250
 ggagactgta ggtttccaga tttcctgaaa aataaaagtt tacagcggtta 2300
 tctctcccca acctcaactaa 2320

<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggctggt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
ggttgagggg ctgcctctgg catatgcaca cactcacaca ttctgtcaca 100
cccgtcacac acacatacca tgttctccat cccccaggt ccagccctca 150
gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
cgtccagtgg gcaggcggtt tcatccctcc tttctctccc aaagcccaac 250
tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300
gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
gttcagcgag cctagagagg gcagactatc agggtgccgg cggtgagaat 400
ccagggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgacaga gccctcagc catgttggga gccaagccac actggctacc 500
 aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550
 tgggggccgg gtggggccag gaggggtcag agcccgctct gctggagggg 600
 gagtgccctg tgggtctgtga gcctggccga gctgctgcag gggggcccgg 650
 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctgcgg 700
 tccgaagcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcgacca ggtcctgggtg aacgagggcg gtggctttga 800
 ccgggcctct ggctccttcg tagccctgt ccgggggtgc tacagcttcc 850
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150
 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250
 gagctgtggc atctccagac caggccttcc caccaccca ccccagtta 1300
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350
 ggcaaggttt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400
 ctccggttcc cccaccccag cttcctgctc aatgctgac agggacaggt 1450
 ggcgaggtg agcctgacag gccccacag gagcccagat ggacaagcct 1500
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctaggggtggg 1600
 aggtcagcc acaggcagaa ggggtgggaag ggcttgaggt ctgtggctgg 1650
 tgaggaagga aggaggggtg attgtctaga ctgaacatgg tacacattct 1700
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
 cactctgact gctgcctcct tctctccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050
 gctgtcttat tctctcctt aggttctcta ttacctggga ttccatgatt 2100
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atggtgggtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser	1	5	10	15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly	20	25	30	
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys	35	40	45	
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly	50	55	60	
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala	65	70	75	
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn	80	85	90	
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu	95	100	105	
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val	110	115	120	
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn	125	130	135	
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val	140	145	150	
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala	155	160	165	
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser				

170

175

180

Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
 185 190 195

Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
 200 205

<210> 288

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-27

<223> Synthetic construct.

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-42

<223> Synthetic construct.

<400> 290

ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50

tagccgcccc gcctcgacgc cgtcccggga cccctgtgct ctgcgcgaag 100

ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150

ttccccgctgg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctcctg cgcgggcgagc gtcaggccga ggctgaccgg 250
 agccagcgct ctcacggagg acctgcgctg tcgcgcgagg ggtctgggag 300
 atggggcact ggatccagca tcctctccgc cctccaggac ctcttctctg 350
 tcacctgggt caataggtcc aagggtgaaa agcagctaca ggtcatctca 400
 gtgctccagt gggctcctgtc cttccttgta ctgggagtgg cctgcagtgc 450
 catcctcatg tacatattct gactgattg ctggctcatc gctgtgctct 500
 acttcacttg gctgggtgtt gactggaaca caccaagaa aggtggcagg 550
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 aacttcagca cagaggccac agaagtgagc aagaagttcc caggcatacg 750
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 acattggttt cgcccatgc atcttccatg gtcgaggcct cttctcctcc 1150
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 agagcccatc accatcccca agctggagca cccaaccag caagacatcg 1250
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 cacaagacca agttcggcct cccggagact gaggtcctgg aggtgaactg 1350
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 tttgctctgt aaatttgaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
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 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu	1	5	10	15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro	20	25	30	
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	35	40	45	
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn	50	55	60	
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	65	70	75	
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile	80	85	90	
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	95	100	105	
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	110	115	120	
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr	125	130	135	
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu	140	145	150	
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile	155	160	165	
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu	170	175	180	
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu	185	190	195	
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser	200	205	210	
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu	215	220	225	
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly	230	235	240	
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	245	250	255	
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly				

260	265	270
Ala Asp Leu Val	Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile	Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln	Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu	Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile	Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His	Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu	Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu	Pro Glu Thr Glu Val Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacctgg ttcccatcta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcttggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcgggcgg atggggggccg ggggcgggcg gcgcccact cgctgaggcc 50
ccgacgcagg gccggggccg gccagggcc gaggagcgcg gcggccagag 100
cggggcccgc gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggcccgtg 250
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtcctg cacggagtgt aactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcacatc 550
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600
gcgcttcgga gtgctgggga gctccaaggt cctcgctaag aaggagctgc 650
tctacgtgcc cctcatcggc tggacgtggt actttctgga gattgtgttc 700
tgcaagcgga agtgggagga ggaccgggac accgtggtcg aagggctgag 750
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800
ggacgcgctt cacggagacc aagcaccgcg ttagcatgga ggtggcggct 850
gctaaggggc ttcctgtcct caagtaccac ctgctgccgc ggaccaaggg 900
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950
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ctctacggga agaagtacga ggcgacatg tgcgtagga gatttcctct 1050
ggaagacatc ccgctggatg aaaaggaagc agctcagtgg cttcataaac 1100
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

tttccagggg agcagtttaa gcctgcccgg aggccgtgga ccctcctgaa 1200
 cttcctgtcc tgggccacca ttctcctgtc tcccctcttc agttttgtct 1250
 tgggcgtctt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300
 tttgtgggag cagcttcctt tggagtctgc agactgatag gagaatcgct 1350
 tgaacctggg aggtggagat tgcagtgagc tgagatggca tcaactgtact 1400
 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaacia 1450
 aaaaacccca gaaattctgg agttgaactg tgtagttact gacatgaaaa 1500
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 agcttgaaga tgggtacctg agatttttca ggctaataaa aaaagaatga 1600
 agggaaatta acagcctcag agacccatgg tgcaccgtca cacaaatcaa 1650
 catatgcatg atgagagtcc cagaaggaga ggagagaaaag ggtcagaaaag 1700
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800
 aatcaaagtg tcaaatgaca aagaatcttg aaagcagcaa gagatgagca 1850
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100
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 gcctcccaaa gtgttgtgat tgcaggcgtg agccactgcg cctggccgga 2250
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 gtgatcccaa gtagcttga ttgtaaacat gcaccacat gcctggctaa 2350
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 gacctcaagt gaccacctgc ctacgcctcc caaagtactg ggattacagg 2450
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 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600

ttgtttctggt gccagggctg gactacagtgc gcacagtctt ggctcactgc 2650
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 agctcaagtgc atctgcctgc ttcagcctcc caaagtgcgtg ggattacaga 2850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccctaacta 2950
 ccaggagagac tgaagtggga ggatcgcttg ggcatgagaa gtcgaggctg 3000
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgcg 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
 80 85 90
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
 95 100 105
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
 110 115 120
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
 125 130 135
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
 140 145 150
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
 155 160 165

Pro	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 298
 cttcctctgt gggtaggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150
tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
tagctgggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggac aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450
tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
ctggcctgac agaattctcat cttgtttaat gctctcataa gaccacttgt 650
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
gttgatatgg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

aggggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950
 gcccagggtg ggcatctcta acaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgata 1100
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
 gcggagggtg cagtgaaccg agatcaggcc actgtattcc aaccagggtg 1300
 acagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 302
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile
 1 5 10 15
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe
 20 25 30
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly
 35 40 45
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val
 50 55 60
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp
 65 70 75
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr
 80 85 90
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln
 95 100 105
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu
 110 115 120
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr
 125 130 135
 Cys Gly Val Leu Leu Ser Phe Leu

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
 aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgctgtgg tggctagtgc tctactcct acctacatta aaatctgttt 200
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350
 ctctcgctgg agcagtgcc tcaccaactg tctcacgtct ggaggcactg 400
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500
 ggcgatggct cccactgccc aggcacacgc cttgctgtag tcaatcactg 550
 ccttggggcc aggcagggcc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgct gcccgcccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700
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 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800
 gtggcagggg aggaacttgt gccaaattat gggtcagaaa agatggaggt 850
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100
 ctcccctcct tccctctgag aggccctcct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgc tcagtgttg cccaggaggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgctccagt aagcacaggc tgcaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
 agctagagct tggttcaa atgatccaag ggcccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750
 aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1				5					10					15
Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20					25					30
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35					40					45
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50					55					60
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
				65					70					75
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
				80					85					90
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
				95					100					105

Arg Arg Arg Asp

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

gcgggccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
tgtaactgcc tcccgcgcgc tctgtcccgc gccatgaccc agccggtgcc 100
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<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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				20					25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
				50					55					60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
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<210> 307

<211> 2272

<212> DNA

<213> Homo sapiens

<400> 307

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<211> 671
<212> PRT
<213> Homo sapiens

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35 40 45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
50 55 60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
65 70 75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
80 85 90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
95 100 105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
110 115 120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
125 130 135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

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	155	160	165		
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala		
	170	175	180		
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu		
	185	190	195		
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala		
	200	205	210		
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys		
	215	220	225		
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	230	235	240		
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser		
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Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln		
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Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly		
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Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu		
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Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser		
	410	415	420		
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg		
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Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	440	445	450
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Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	485	490	495
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	500	505	510
Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	515	520	525
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Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	590	595	600
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	605	610	615
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	620	625	630
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	635	640	645
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	650	655	660
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 <212> DNA
 <213> Homo sapiens

<400> 309
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<210> 310
 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
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 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
 50 55 60
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
 65 70 75
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

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Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
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Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
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Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
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Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe	410	415	420
Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	425	430	435
Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr	440	445	450
Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp	455	460	465
Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val	470	475	480
Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu	485	490	495
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu	500	505	510
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly	515	520	525
Leu	Val	Gln	Leu	Ser	Leu	His	Arg	Cys	Asp	Thr	Tyr	Gly	Lys	Ala	530	535	540
Cys	Ala	Asp	Cys	Cys	Leu	Ala	Arg	Asp	Pro	Tyr	Cys	Ala	Trp	Asp	545	550	555
Gly	Asn	Ala	Cys	Ser	Arg	Tyr	Ala	Pro	Thr	Ser	Lys	Arg	Arg	Ala	560	565	570
Arg	Arg	Gln	Asp	Val	Lys	Tyr	Gly	Asp	Pro	Ile	Thr	Gln	Cys	Trp	575	580	585
Asp	Ile	Glu	Asp	Ser	Ile	Ser	His	Glu	Thr	Ala	Asp	Glu	Lys	Val	590	595	600
Ile	Phe	Gly	Ile	Glu	Phe	Asn	Ser	Thr	Phe	Leu	Glu	Cys	Ile	Pro	605	610	615
Lys	Ser	Gln	Gln	Ala	Thr	Ile	Lys	Trp	Tyr	Ile	Gln	Arg	Ser	Gly	620	625	630
Asp	Glu	His	Arg	Glu	Glu	Leu	Lys	Pro	Asp	Glu	Arg	Ile	Ile	Lys	635	640	645
Thr	Glu	Tyr	Gly	Leu	Leu	Ile	Arg	Ser	Leu	Gln	Lys	Lys	Asp	Ser	650	655	660
Gly	Met	Tyr	Tyr	Cys	Lys	Ala	Gln	Glu	His	Thr	Phe	Ile	His	Thr			

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu	
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu	
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu	
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp	
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp	
740	745	750
Lys His Met Gln Glu Met Lys Lys Lys	Arg Asn Arg Arg His His	
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala	Val Ala Thr	
770	775	

<210> 311
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 311
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<210> 312
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 313
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<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				

	305		310		315
Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro	Gly		
	320	325	330		
Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met	Ala Pro		
	335	340	345		
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala	Lys Ala		
	350	355	360		
Pro Asp Pro Gly	His Pro Asp Pro	Leu Thr			
	365	370			

<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
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<210> 317
<211> 837
<212> PRT
<213> Homo sapiens

<400> 317

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			20						25					30
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
			35					40					45	
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
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Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu

140										145					150				
Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu					
				155					160					165					
Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile					
				170					175					180					
Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn					
				185					190					195					
Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala					
				200					205					210					
Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val					
				215					220					225					
Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg					
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Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His					
				245					250					255					
Pro	Ser	Ile	Arg	Asn	Pro	Val	Ser	Leu	Val	Val	Thr	Arg	Leu	Val					
				260					265					270					
Ile	Leu	Gly	Ser	Gly	Glu	Glu	Gly	Pro	Gln	Val	Gly	Pro	Ser	Ala					
				275					280					285					
Ala	Gln	Thr	Leu	Arg	Ser	Phe	Cys	Ala	Trp	Gln	Arg	Gly	Leu	Asn					
				290					295					300					
Thr	Pro	Glu	Asp	Ser	Gly	Pro	Asp	His	Phe	Asp	Thr	Ala	Ile	Leu					
				305					310					315					
Phe	Thr	Arg	Gln	Asp	Leu	Cys	Gly	Val	Ser	Thr	Cys	Asp	Thr	Leu					
				320					325					330					
Gly	Met	Ala	Asp	Val	Gly	Thr	Val	Cys	Asp	Pro	Ala	Arg	Ser	Cys					
				335					340					345					
Ala	Ile	Val	Glu	Asp	Asp	Gly	Leu	Gln	Ser	Ala	Phe	Thr	Ala	Ala					
				350					355					360					
His	Glu	Leu	Gly	His	Val	Phe	Asn	Met	Leu	His	Asp	Asn	Ser	Lys					
				365					370					375					
Pro	Cys	Ile	Ser	Leu	Asn	Gly	Pro	Leu	Ser	Thr	Ser	Arg	His	Val					
				380					385					390					
Met	Ala	Pro	Val	Met	Ala	His	Val	Asp	Pro	Glu	Glu	Pro	Trp	Ser					
				395					400					405					
Pro	Cys	Ser	Ala	Arg	Phe	Ile	Thr	Asp	Phe	Leu	Asp	Asn	Gly	Tyr					
				410					415					420					
Gly	His	Cys	Leu	Leu	Asp	Lys	Pro	Glu	Ala	Pro	Leu	His	Leu	Pro					
				425					430					435					

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln	440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro	455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala	470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys	485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp	500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro	515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val	530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly	545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn	560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu	575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe	590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro	605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr	620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser	635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala	650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys	665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly	680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile	695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro	710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser			

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cgggtgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320

ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

cagcagtggg ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50

gagagacat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100

ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150

ttgtggactg gtgtttggta tcctggccct aactctaatt gtctgtttt 200

gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250

gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300

tgatcctgtg accagaactg aaatattcag aagcggaaat ggactgatg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400

gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450

attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500

ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550

aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600

gaccatgtat tggatcaatc ccactctaatt atcagtttct gagttacaag 650

actttgagga ggaggagaa gatcttcact ttctgcca cgaaaaaaaa 700

gggattgaac aaaatgaaca gtgggtggtc cctcaagtga aagtagagaa 750

gacccgtcac gccagacaag caagtgagga agaacttcca ataatgact 800

atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850

tgttgtatth actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900

acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950

tcactctgtc tgtcatcatg ccttgtaact ggtgggtggc ccgcatgctg 1000

gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050

atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100

cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150

tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
 275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
 290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
 305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

gcggaactgg ctccggctgg cacctgagga gcggcgtagc cccgagggcc 50
 cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100
 ggccgtgcag cttctgggct tctgtctcag cttcctgggc atggtgggca 150
 cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtgggc 200
 accaacaatcc tcacggccgt gtctactctg aaagggctct ggatggagtg 250
 tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300
 tggcgctgcc ccaagacctc cagggtgccc gcgccctcat ggtcatctcc 350
 tgctgtctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400
 cacgcgtgac gccaaagggca caccgcgcaa gaccaccttt gccatcctcg 450
 gcggcaccct cttcatcctg gccggcctcc tgtgcatggt ggccgtctcc 500
 tggaccacca acgacgtggt gcagaacttc tacaaccgcg tgctgcccag 550
 cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600
 cgtccctctc gctcattggt ggcaccctgc tttgcctgtc ctgccaggac 650
 gaggcaccct acaggcccta ccaggccccg cccagggcca ccacgaccac 700
 tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
 gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800
 tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850
 gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900
 ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950
 ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100
gtttggtcag tgggggttgg ttgtgatcca ggaataaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324
<211> 239
<212> PRT
<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
 gagctcccct caggagcgcg ttagcttcac accttcggca gcaggagggc 50
 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200
 aaccccgta cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
 gtcttggtg ccattggcct cctggtatcc atctttgcc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggtcttt gtgcaattgc tggagtgtct 500
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 ggggggtgtga tgatgtgcat cgcctgccgg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgcccgcaca gaggacgagg tacaatctta 850
 tccttccaag cagcactatg tgtaatgtc taagacctct cagcacgggc 900
 ggaagaaact cccggagagc tcacccaaaa aacaaggaga tcccatctag 950
 atttcttctt gcttttgact cacagctgga agttagaaaa gcctcgattt 1000
 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaat ataactttct actctgatga 1150
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200
 cccctcttc ctctagtca ataaacccat tgatgatcta tttcccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
 ttctgctggt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400
 cccatgatct cggtttttctt aactgtgat cttaaaagt accaaacca 1450
 agtcattttc agtttgaggc aaccaaact ttctactgct gttgacatct 1500
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550
 tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600
 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
 taaaatgata cactatctct gtgaaatagc ctcacccta catgtggata 1700
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
 agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950
 gaggctgagg tgggaggatc acttgagccc agggagggtg gggctgcagt 2000
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
 gtctaaaaaa ataaaaata aataatggaa cacagcaagt cctaggaagt 2100
 aggttaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1				5					10					15
Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
				245					250					255					
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327
 <211> 2010
 <212> DNA
 <213> Homo sapiens

<400> 327
 ggaaaaactg ttctcttctg tggcacagag aaccctgctt caaagcagaa 50
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
 gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggttt catgatggcc atccttggca 400
 tgaaatgcac caggtgcacg ggggacaatg agaaggtgaa ggctcacatt 450
 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500
 ccctgtgagc tgggttgcca atgccatcat cagagatttc tataactcaa 550
 tagtgaatgt tgcccaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttgga ggagctctgt tctgctgcgt 650
 tttttgttgc aacgaaaaga gcagtagcta cagatactcg ataccttccc 700
 atcgcacaac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagttgtgt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggaccc 850
 caaagaaact ttgatttact gttcttaact gcctaattct aattacagga 900
 actgtgcac agctatttat gattctataa gctatttcag cagaatgaga 950
 tattaaaccc aatgctttga ttgttctaga aagtatagta atttgttttc 1000
 taagggtggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattatit tactactgta atttctccac gacatagcat 1100
 tatgtacata gatgagtgtg acatttatat ctcacataga gacatgctta 1150
 tatgggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200
 actcaactat tgctttttcag ggaaatcatg gatagggttg aagaagggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300
 gaagattaaa atgaaggctt taatcagcat tgtaaaggaa attgaatggc 1350
 tttctgatat gctgtttttt agcctaggag ttagaaatcc taacttcttt 1400
 atcctcttct ccagagggt ttttttttct tgtgtattaa attaacattt 1450
 ttaaaacgca gatattttgt caaggggctt tgcattcaaa ctgcttttcc 1500
 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550
 gttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650
 gagtacagac tttgagggtt catcaatata aataaaagag cagaaaaata 1700
 tgtcttggtt ttcatttgct taccaaaaaa acaacaaca aaaaagttgt 1750
 cctttgagaa cttcacctgc tcctatgtgg gtacctgagt caaaattgtc 1800

atttttggtc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
 tcgccatggc ctctgccgga atgcagatcc tgggagtcgt cctgacactg 50
 ctgggctggg tgaatggcct ggtctcctgt gccctgccca tgtggaaggt 100
 gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150
 gcctgtggat gtctgcgtg gtgcagagca cgggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgtgggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgctggtgc tcacctctgg gattgtcttt gtcattctcag gggctcctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggg ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg ccttttggtg ctgggtgggg ggttgctgtg 550
 ctgcacttgc ccctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc acccttggtg gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttagaagc cagtcaagct atggaactaa 950
 tgcggaggct gcttgctgtg ctggctttgc aacaagacag actgtcccca 1000
 agagtctctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gtgcccccc atcctactca ggtctctgga gctcctctct tcaccctgg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgtttc ctccgtctg ataagacgtc cccccccag ggccaggtcc 1200
 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250

gccccctcg tctcaccccc ttacactca catttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

gccaaggaga acatcatcaa agacttctct agactcaaaa ggcttccacg 50
ttctacatct tgagcatctt ctaccactcc gaattgaacc agtcttcaaa 100
gtaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttgg 150
gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200
ggagtatcag cttttgttgg cagcaacatt attgtctttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctccttg ttggtctctc cgctgcctt ggaaacagcc 350
cgggccctca tgtgtgtggc tgttgcctc tccttgatcg ccctgcttat 400
tggcatctgt ggcatgaagc aggtccagtg cacaggctct aacgagaggg 450
ccaaagcata ccttctggga acttcaggag tcctcttcat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
cacttttctt tggctgggca agcgtgctg tcctcttcat tggaggggggt 650
ctgctttgtg gattttgtg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaattgct ccttttggct 800
ccaagtatgg actatgggtc atgtttttta taaagtcctg ctagaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtttc aatttgttac tgggtggtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgta ttaaattgcat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtataccca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

1	5	10	15
Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg	20	25	30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu	35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn	50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe	65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala	80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly	95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser	110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys	125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly	140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu	155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
 agtgacaatc tcagagcagc ttctacacca cagccatttc cagcatgaag 50
 atcactgggg gtctccttct gctctgtaca gtggtctatt tctgtagcag 100
 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

cccgcgcccc gttctccctc gcagcacctc gaagtgcgcc cctcgccctc 50

ctgctcgcgc cccgcgcgca tggctgcctc cccgcgcgcg cctgctgtcc 100

tggccctgac cgggctggcg ctgctcctgc tctgtgtctg gggcccaggt 150

ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550

agcgattctc ttcattgtatc tctaattgcc ttacactact tggtttctga 600

tttgccttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gaagagttaa aacaacacat gtaaatacct tttgatattt catgggaatg 700
 cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 336
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
 1 5 10 15
 Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145 "

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
 cggctcgagc ccgcccggaa gtgcccagg ggccgcgatg gagctggggg 50
 agccgggagc tcggtagcgc ggcgggcaag gcaggcgcca tgaccctgat 100
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150
 ttctgggtgct ggcccttgcc tgggtctcaa cgacacccgc tgagggcggg 200
 gacccaactgc ccagccgctc agggacccca acgcatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 cccccagcct gagacacaga ggtcaagctg cacagccaga gccagcacg 350
 gggttcacag caacaccgcc agccccggac tccccgcagg agcccctcgt 400
 gctacggctg aaattcctca atgattcaga gcagggtggcc agggcctggc 450
 cccacgacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 gaccctgggc agccttcacc tccctcccaa ctgcgtttct cactgccacg 600
 tgtccacgag agtcggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 cccggcccct cggggtgga aatcggcagc ctgctgctgc ccctgctgct 700
 cctgctgttg ctgctgctct ggtactgcca gatccagtac cgccccttct 750
 ttcccctgac cgccactctg ggcctggccg gcttcaccct gctcctcagt 800
 ctcttgccct ttgccatgta ccgcccgtag tgcctccgag ggcgcttggc 850
 agcgtcgccg gccctcccg accttgctcc ccgcgccgag gcgggagctg 900
 ctgcctgcc agggccgcct ctccggcctg cctcttcccg ctgccctgga 950
 gccagccct gcgcgcgaga ggactcccgg gactggcgga ggccccgccc 1000
 tgcgaccgcc ggggctcggg gccacctccc ggggctgctg aacctcagcc 1050
 cgcaactggga gtgggctcct cggggtcggg catctgctgt cgctgcctcg 1100
 gccccgggca gagccggggc gccccggggg cccgtcttag tgttctgccc 1150
 gaggaccag ccgctccaa tcctgacag ctccctgggc tgagttgggg 1200
 acgccaggtc ggtgggaggc tggggaaggg gagcggggag gggcagagga 1250
 gttccccgga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
 aaaaaaaaa 1310

<210> 338
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5					10					15
Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
				20					25					30
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35					40					45

Thr Pro Thr Pro Ser Gln Pro Ser Ala Ala Met Ala Ala Thr Asp
 50 55 60
 Ser Met Arg Gly Glu Ala Pro Gly Ala Glu Thr Pro Ser Leu Arg
 65 70 75
 His Arg Gly Gln Ala Ala Gln Pro Glu Pro Ser Thr Gly Phe Thr
 80 85 90
 Ala Thr Pro Pro Ala Pro Asp Ser Pro Gln Glu Pro Leu Val Leu
 95 100 105
 Arg Leu Lys Phe Leu Asn Asp Ser Glu Gln Val Ala Arg Ala Trp
 110 115 120
 Pro His Asp Thr Ile Gly Ser Leu Lys Arg Thr Gln Phe Pro Gly
 125 130 135
 Arg Glu Gln Gln Val Arg Leu Ile Tyr Gln Gly Gln Leu Leu Gly
 140 145 150
 Asp Asp Thr Gln Thr Leu Gly Ser Leu His Leu Pro Pro Asn Cys
 155 160 165
 Val Leu His Cys His Val Ser Thr Arg Val Gly Pro Pro Asn Pro
 170 175 180
 Pro Cys Pro Pro Gly Ser Glu Pro Gly Pro Ser Gly Leu Glu Ile
 185 190 195
 Gly Ser Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu Leu
 200 205 210
 Trp Tyr Cys Gln Ile Gln Tyr Arg Pro Phe Phe Pro Leu Thr Ala
 215 220 225
 Thr Leu Gly Leu Ala Gly Phe Thr Leu Leu Leu Ser Leu Leu Ala
 230 235 240
 Phe Ala Met Tyr Arg Pro
 245

<210> 339
 <211> 849
 <212> DNA
 <213> Homo sapiens

<400> 339
 gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50
 tgccctctcc agattcccca ggctctcaga gaagatcagc agaaagtctg 100
 caagacccta agaaccatca gccctcagct gcacctcctc cctccaagg 150
 atgacaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200
 tcaggccagc ctcacagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttggg tgggtttgag ggttactccc tgagtgactg gctgtgcctg 300
 gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tggaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
 acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gtccggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550
 caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
 aggggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
 ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
 ccttccatt tacaactaaa actgaccaga gcccaggaa taaatgggtt 750
 tcttggttc ctccttactc ccattctggac ccagtcacct ggttctgtc 800
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
 1 5 10 15
 Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
 20 25 30
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
 35 40 45
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
 50 55 60
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
 65 70 75
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
 80 85 90
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
 95 100 105
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
 110 115 120
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
 125 130 135
 Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 345

agctttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

tctgacctga ctggaagcgt ccaaagaggg acggctgtca gccctgcttg 50

actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100

caaaggggga aagaaacacc tgagcagaat ggaatcatta tttttttccc 150

aaggagaaaa ccggggtaaa gggagggag caattcaatt tgaagtcct 200

gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250

gggggtgaaac ttgggtcctg tgggtttctg attgtaagtg gaagcaggtc 300

ttgcacacgc tgttggcaaa tgcaggacc aggttaagtg actggcagaa 350

aaacttccag gtggaacaag caacccatgt tctgtctcaa gcttgaagga 400

gcctggagcg ggagaaagct aacttgaaca tgacctgttg catttgga 450

gttctagcaa catgctcta aggaagcgat acaggcacag accatgcaga 500

ctccagttcc tctgtctgct cctgatgctg ggatgcgtcc tgatgatggt 550

ggcgatgttg caccctcccc accacaccct gcaccagact gtcacagccc 600

aagccagcaa gcacagccct gaagccagggt accgcctgga ctttggggaa 650

tcccaggatt ggggtactgga agctgaggat gaggggtgag agtacagccc 700

tctggagggc ctgccaccct ttatctcact gcgggaggat cagctgctgg 750

tggccgtggc cttaccccag gccagaagga accagagcca gggcaggaga 800

ggtgggagct accgcctcat caagcagcca aggaggcagg ataaggaagc 850

cccaaagagg gactgggggg ctgatgagga cggggagggt tctgaagaag 900

aggagttgac cccgttcagc ctggaccac gtggcctcca ggaggcactc 950

agtgcccgca tccccctcca gagggctctg cccgagggtgc ggcacccact 1000

gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050

tctgtttcca tgatgaggcc tggtcactc tctgcggac tgtacacagc 1100

atcctcgaca cagtgccag ggccttcctg aaggagatca tcctcgtgga 1150
 cgacctcagc cagcaaggac aactcaagtc tgctctcagc gaatatgtgg 1200
 ccaggctgga gggggtgaag ttactcagga gcaacaagag gctgggtgcc 1250
 atcagggccc ggatgctggg ggccaccaga gccaccgggg atgtgctcgt 1300
 cttcatggat gccactgcg agtgccaccc aggctggctg gagcccctcc 1350
 tcagcagaat agctggtgac aggagccgag tggatatctcc ggtgatagat 1400
 gtgattgact ggaagacttt ccagtattac ccctcaaagg acctgcagcg 1450
 tggggtgttg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
 atgtgaggaa ggccctccag tccccataa gcccacatcag gagccctgtg 1550
 gtgcccggag aggtggtggc catggacaga cattacttcc aaaacactgg 1600
 agcgtatgac tctcttatgt cgctgcgagg tggtgaaaac ctggaactgt 1650
 ctttcaaggc ctggctctgt ggtggctctg ttgaaatcct tccctgctct 1700
 cgggtaggac acatctacca aaatcaggat tccattccc ccctcgacca 1750
 ggaggccacc ctgaggaaca gggttcgcat tgctgagacc tggtgggggt 1800
 cattcaaaga aaccttctac aagcatagcc cagaggcctt ctccttgagc 1850
 aaggctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
 gggttgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
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 acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150
 gctgtcaggc aggagcaggc gattcttcag aactgcacgg aggaaggcct 2200
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 aagagaattt tggccatcaa aatccagctc caagtgaacg taaagagctt 2450
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala	Val Arg Gln Glu Gln Val	
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly	Leu Ala Ile His Gln Gln	
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met	Ile Val His Ile Leu Ser	
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln	Glu Asn Asn Lys Asp Leu	
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg Phe	
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 348
 ggagaggtgg tggccatgga cag 23

<210> 349
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 349
 ctgtcactgc aaggagccaa cacc 24

<210> 350
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 350
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<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tcctctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccgctgtg 200
caggggaggg ccctcgcccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcttg 300
cctggcactg cacccccagc caccatca ggctttgagg aggggccgcc 350
ctcatcccaa taccctggg ctatcgtgtg gggcccacc gtgtctcgag 400
aggatggagg ggacccaac tctgccaatc ccggatttct ggactatggt 450
tttgagccc ctcatgggct cgcaaccca caccacaact cagactccat 500
gcgaggtgat ggagatggg ttatccttgg agaggcacct gccaccctgc 550
ggccattcct gttcgggggc cgtggggaag gtgtggacct ccagctctat 600
gtcacaatta ccatctccat catcattgtt ctctgggcca ctggcatcat 650
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
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caccctgac catgaggagc ccgaggggg accccggcct gggatgcccc 850
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 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10					15

Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
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tccgggggttc tggcccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggtecccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggcggtcgc tggggcccg cgctatcgc gccatcgtga 350
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
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 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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 gttggccggc ggccggccgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
 tctccaagaa gttctccttc taccgccacc atgtgaactt caagtccctgg 200
 tgggtgggcg acatccccgt gtcaggggcg ctgctcaccg actggagcga 250
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
 agaagctgga ccaagtggcg acagcagtgt accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
 catcttccgg gagcaggtgc acctcatcca gaacgccatc atcgaaaggc 450
 acctggcacc aggcagctgg ggaggagggc agctctccag ggagggaccc 500
 agcctagcac ctgaaggatc aatgccatca ccccgcgggg acctccccta 550
 agtagcccc agaggcgctg ggagtgttg caccgccctc ccctgaagtt 600
 tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggccc 650
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 tggcatcttc cagtacgaga ccatctcctg caacaactgc acagactcgc 750
 acgtgcctg ctttggctat aactgcgagt agggctcagg catcacaccc 800
 acccgtgcca gggccctact gtccctgggg tcccaggctc tccttgagg 850
 gggctccccg ccttcacact ggctgtcatc gggtagggcg gggccgtggg 900
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 cgggcatctt tcctaaagg tcccatagg gtctggttcc acccatccc 1250
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cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
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 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggaggagg 2050
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1 5 10 15
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 " 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
 125 130 135
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357
<211> 1536
<212> DNA
<213> Homo sapiens

<400> 357
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cctcttattt ctcctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcagatggg cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgccc atactccata 250
gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctcctcctga taatgaacaa ggcctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctcttttattc tgggtggacag tggatgaaa gaaaatggga aggtgatatc 650
atcttttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
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ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
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acacacacac gcacgtgcac acacgcacgc acgctgtcac acacacacgc 1000
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tctcttcttc cttcttttaa atttcatatc ctcactccct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
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ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggtgtctc caagtccttg aactcagcag aaatagacca 1450
tgtgaaaact ccattgcttg ttagcatctc caactcccta tgtaaatcaa 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
1 5 10 15

Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
20 25 30

Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45

Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60

Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75

His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90

Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105

Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120

Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135

Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150

Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180

Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagtgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga ggcggcgctg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccca ggcgagccaa 100
cctcagcggg gaccgggct caggacgcg gcggcgcgcg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggg gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca aggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcgagc atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150
 cctgatatga ggagccagtg ttgcatgatg aaaagatggg atgattctac 1200
 atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
 ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500
 ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600
 tttgcacct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	
				110					115					120	
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	
				125					130					135	
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	
				140					145					150	
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	
				155					160					165	
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	
				170					175					180	
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	
				185					190					195	
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	
				200					205					210	
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	
				215					220					225	
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	
				230					235					240	
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	
				245					250					255	
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		
				260					265						

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacgcc atgtaccggc tctgtcagc agtgactgcc 50
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
 ccatcagcgc gccgggctgc cgctctcgg ccacggctgg gtcggggggc 150
 tcgggctggg gctggggctg gcgctcggg tgaagctggc aggtgggctg 200
 aggggcgcgg ccccggcgca gtccccgcg gccccgacc ctgaggcgtc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccg 300
 agaccccggc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
 agtggttga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 agattactga ttccccattt aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
 ttcaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggc aatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct gtaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5					10					15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20					25					30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35					40					45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50					55					60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65					70					75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80					85					90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val	350	355	360
Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg	365	370	

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagagaa gtctgggtcag aaggtttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcaac ccggtctctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200
 tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
 tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
 tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
 gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
 gaagctggtg gctatgtctc ctcctttgtc cctgcgtgct ccctggtgga 500
 gtgcacactg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
 tgggtggcgt gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
 gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagegcctgg 700
 agatggaaca ggcccagaag gccagaacc ccaggagca gaagtccttc 750
 ttgcgcaaat actggatgta catcattccc gtgctcctgt tcctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatacgta ttcagaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaaacccga gccggagccg gagccacagc ggggaggggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggtcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctgggggt ggaactgtca agatgccggg 200

ctaaaccccc tggaagggcc tgcagcaatc cctccttccct tcggtttcaa 250
 ctggacttct atcagggtcta ctccctggcc ctggcagctg attggcttca 300
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
 aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
 ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
 cctcttctcc ctgacttact cactatgctg cttaaccaaa ctctctcaag 500
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
 ctgctcttct cagccttcga ggccctggat atccatgagc acgtggaacg 600
 gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
 tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
 gccagctgga tagggctggg gcctgtagcg ccttttgtgg ctgccatccc 750
 tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
 atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
 ctctgtcgg accgcgcgt gctgctgctg ggcaccatac aagctctatt 900
 tgagagtgtc atcttcatct ttgtcttccct ctggacacct gtgctggacc 950
 cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
 ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
 tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
 tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
 tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
 cagcatgagc ttctacgga gaaaggtgat ccctgagaca gagcaggctg 1250
 gtgtactcaa ctggttcggt gtacctctgc actcactggc ttgcctaggg 1300
 ctccctgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
 cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
 tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
 gaggagccct atgcccctga gctgtaaccc cactccagga caagatagct 1500
 gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile	245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp	260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe	275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg	290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu	305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr	320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile	335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser	350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala	365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys	380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr	395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu	410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu	425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu	440	445	450

<210> 375
 <211> 1098
 <212> DNA
 <213> Artificial

<400> 375
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50
 gccctggaga tggccccgg cgccgcgggc tgggtgtgtc tcgtgctctg 100
 gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 cctgccaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300
 tcttcatcca ggaccagatt gctctggtgg agagggggggg ctgctccttc 350
 ctctccaaga ctcggtggt ccaggagcac ggcgggcggg cggatgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagtaccca gcgcacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccgccg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
 aatttgaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttccttc 800
 cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
 cccagggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
 taccagggt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10						15
Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
				20				25						30
Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
				35				40						45
Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
				50				55						60
Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
				65				70						75
Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
				80				85						90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctctccta 150
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacgg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val	1	5	10	15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys	20	25	30	
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly	35	40	45	
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr	50	55	60	
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys	65	70	75	
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile	80	85	90	
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe	95	100	105	
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu	110	115						

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt cttcttgat gggggcccag gggggccagg agagtataaa 50
ggcgatgtgg agggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccataaatac acagggtctg 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
ctttcctccg gggatgggtc atgtacacca gcaaggaccg ctatttctat 450
tttggaagc ttgatggcca gatctctctt gcctacccca gccaaaggagg 500
gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcataaga 550
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650
ggatatggggc catccgagct gaggccatct gtgtgggtgt ggctgatgt 700
actggagtaa ctgagtcggg acgtgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5					10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
				20					25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
				35					40					45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln	50	55	60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly	65	70	75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr	80	85	90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met	95	100	105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly	110	115	120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val	125	130	135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly	140	145	150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro	155	160	165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg			170	175	

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
 gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50
 agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
 tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350
 atgttcctaaa atcgttccat ctccaagggt gtccaatttt tcttcctggg 400
 tgtcagcgag cctgactca ctacagtgc gctgacagg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
 acaaaggatg gggtttcaatg taattaggct actgagcgga tcagctgtag 550
 cactgggtat agccccact gtcttactga caatgctttc ttctgccgaa 600
 cgaggatgcc ctaagggtg taggtgtgaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tatactctgct ggttgcttag 700
 gtttgccctc togtataaac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttggacct gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
 cagaaccttt acttgcaagt gaataaaatc agtgtcatag gacagaccat 1250
 gtcctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggaccc agtggtttcc agtgtgtccc gaatctgcag 1350
 cgcctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggtc tcccaaagcc gacgtttaag 1650
 cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgcccccgac 1700
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800
 ctcgatcatc tgctggttat ctacgtgtca tggaagcggg accctgcgag 1850
 catgaagcag ctgcagcagc gtcctcat gcgaaggcac aggaaaaaga 1900
 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggaccctgc acctataaca aatcgggctc caggagagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaagct gggaaataag tgggtgctta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150
 tctccctctc actttggtgg caagatcctt ccttgtccgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcatth gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

200					205					210				
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe
				215										225
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys
				230										240
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu
				245										255
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly
				260										270
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu
				275										285
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser
				290										300
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu
				305										315
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe
				320										330
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu
				335										345
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile
				350										360
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu
				365										375
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu
				380										390
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly
				395										405
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile
				410										420
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu
				425										435
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys
				440										450
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys
				455										465
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr
				470										480
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu
				485										495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
 ggtccccagg acatggtctg tccc 24

<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtaacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcggaacct ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctgggtat atctggatcc tcctgctgct ggTTTTggtg 250
 gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
 gagacccoga attgattctc acaggcgcac catggcagtt tttgctggtg 350
 gagacttggg ctctatttat gggacagaag cagctgtgag tccaactgtt 400
 ggaattcacc ttcaaaactca aacccttgac ctatatcctg ttctgctcc 450
 atgttttggc cctttaggct cccacctcc atatgaagaa attgtaaaaa 500
 caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
 taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
 tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
 ggatgttggg aaaaattttg gtcattggaga tgtttaata gtaaagtagc 700
 aggcttttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
 attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
 gtagtttcca tcacatttag gactccactg cagtatacag cacaccatTT 850
 tctgctttaa actctttcct agcatggggT ccataaaaat tattataatt 900
 taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
 agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
 tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
 gtctcagcaa aaacaagagg ttttatgccc caacctgaag aggaagaaat 1100
 tgtagataga aggtgaagga gattgctgaa gatatagagc acatataatg 1150
 ccaacacggg gagaaaagaa aatttcccct tttacagtaa tgaatgtggc 1200
 ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
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 agcaggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
 ctgacaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5					10				15	

Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
				35					40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
				50					55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
				65					70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 391
 cttttcagtg tcacctcagc gatctc 26

<210> 392
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 392
 ccaaaacatg gagcaggaac agg 23

<210> 393
 <211> 47
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50
accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcgggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctctttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatgtggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600
tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700
attttgcaac gattggtgaa gctggagaac aaagttgact atattgttgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttgggtgc 800
cagtaaccac aaataaaaga acgaatgtct cgggcagtat cagatagcag 850
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttaacaata 950
aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaatth ggtaacttgg ttgatgtggt 1100

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agtatataac acgttttttg gacaagtga gaagtgttaa tcattctgtc 1250
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tgcttattgt actatatttt gttattccaa ttatgagcag agaaaggaaa 1350
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tacttttgtg ctgcattaaa ttgcttgga agtggttaaca ttatattata 1850
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tatgaagatt gactatcttt tcaggaaaaa agctgtatat agcacaggga 2000
accctaactc tgggtaattc tagtataaaa caaattatac ttttatttaa 2050
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catgtagcaa taattacaat attttattaa aataaatatg tgaaatattg 2250
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acctttatgt gaagaaatta atttatgccc attgccaggt 2340

<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	

Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
 cgcgccggg ccgcccgggt gagcgtgccg aggcggctgt ggcgcaggct 50
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 gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150
 accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200
 cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250
 tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
 gggccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350
 caccagcatc tcacccactg ccttctcccc ccttcgctac ctggagtcgc 400
 ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450
 agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500
 ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550
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 ggctgctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650

ccattgccgtg cccaacctcc gagacttgcc cctgcgctac ctgagcctgg 700
 atgggaaccc tctagctgtc attgggtccgg gtgccttcgc ggggctggga 750
 ggccttacac acctgtctct gccagcctg cagaggtcc ctgagctggc 800
 gccagtggc ttccgtgagc taccgggcct gcaggtcctg gacctgtcgg 850
 gcaaccccaa gcttaactgg gcaggagctg aggtgttttc aggctgagc 900
 tccctgcagg agctggacct ttcgggcacc aacctggtgc cctgcctga 950
 ggcgtgctc ctccacctcc cggcactgca gagcgtcagc gtgggccagg 1000
 atgtgcggtg ccggcgctg gtgcgggagg gcacctacc ccggaggcct 1050
 ggctccagcc ccaagggtgcc cctgcactgc gtagacacc gggaatctgc 1100
 tgccaggggc ccacatct tgtgacaaat ggtgtggccc agggccacat 1150
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 tctcagcttc cgaaccctgg gctgtttcct tagtcttcat ttataaaaag 2300
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 tttgttcaact tttgtaatat tgtcctgggc ctgtgttggg gtgttggggg 2450
 aagctgggca tcagtggcca catgggcac aggggctggc cccacagaga 2500
 cccacaggg cagtgaagctc tgtcttcccc cacctgccta gcccatcatc 2550
 tatctaaccg gtccttgatt taataaacac tataaaaagg ttataaaaaa 2600
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 397
 Met Pro Trp Pro Leu Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
 1 5 10 15
 Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
 20 25 30
 Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
 35 40 45
 Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
 50 55 60
 Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
 65 70 75
 Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
 80 85 90
 Leu Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser
 95 100 105
 Arg Leu Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu
 110 115 120
 Thr Ala Leu Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp
 125 130 135
 Val Asn Leu Ser His Asn Gln Leu Arg Glu Val Ser Val Ser Ala
 140 145 150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly Pro Thr Ile Leu	350		

<210> 398
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 398
 ccctgccagc cgagagcttc acc 23

<210> 399
 <211> 23
 <212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caaccccaag cttactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatggcgag ccacagcttc tgtgagattc gatttctccc cagttcccct 50

gtgggtctga ggggaccaga aggggtgagct acgttggctt tctggaagg 100

gaggctatat gcgtcaattc cccaaaacaa gttttgacat ttcccctgaa 150

atgtcattct ctatctattc actgcaagt cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400

ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcgaaatcga 600

tgctgcctcc tgcgpcattt gctaagactc tatctggaca gggatattta 650

aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700

ccaattcctt tcttaccatc aagaaggacc tccggtctc tcatgcccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcacatgac ccaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tcacagtgtg tcttatttat gcattacttg cttccttgca 1050
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 tttttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
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 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tttttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
1				5					10					15
Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20					25						30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35					40						45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
			50					55						60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65					70						75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80					85						90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-28
 <223> Synthetic construct.

<400> 403
 ctctgtggt ctccagattt caggccta 28

<210> 404
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 404
agtcctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50
aggcttttgc cgctgacca gagatggccc cgagcgagca aattcctact 100
gtccggctgc ggggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgcac ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tcccccttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttgggcag 600
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
accacttatg atacagtga acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgaccc cttggtcaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30.
 Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45
 Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60
 Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75
 Leu Gly Ile Ile Glu Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90
 Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105
 Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120
 Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135
 Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165
 Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180
 Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195
 Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210
 Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225
 Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240
 Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255
 Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270
 Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285
 Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300
 Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-31
<223> Synthetic construct.

<400> 407
cgcggatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-34
<223> Synthetic construct.

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50
tcttgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100
cagcatttaa tgaaaaatct atgcttaaga agtaaaaatg gcaggcttcc 150
tagataatct tcgttggcca gaatgtgaat gtattgactg gagtgagaga 200
agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatctt ccacattggc tttcttcatg 350
ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400
ctgttttagga agaacagggtg ctcgagtttg gcttttcatt ggtttcatgt 450
tgatgtttgg gtcacttatt gcttccatgt ggattctttt tggatcatat 500
gttaccctaaa atactgatgt ttatccggga ctagctgtgt tttttcaaaa 550

tgcacttata ttttttagca ctctgatcta caaatttga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttcct tttgttatat 650
 tctgtttgta gataggtttt ttatctctca gtacacattg ccaaattggag 700
 tagattgtac attaaatggt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattcctgag atttagaact tgatctactc cctgagccag ggttacatca 900
 tcttgtcatt ttagaagtaa ccactcttgt ctctctggct gggcacggtg 950
 gctcatgcct gtaatccag cactttggga ggccgaggcg ggccgattgc 1000
 ttgaggtcaa gtgtttgaga ccagcctggc caacatggcg aaaccccatc 1050
 tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
 aggttgagcgt gagctgagtt tgcgccactg cactctagcc tggggggagaa 1200
 agtgaaactc cctctcaaaa aaaagaccac tctcagtatc tctgatttct 1250
 gaagatgtac aaaaaaatat agcttcatat atctggaatg agcactgagc 1300
 cataaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtg aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
 tttatataat gattttttta atgcccaaag gactagtttg aaagcttctt 1450
 ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 410
 Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
 1 5 10 15
 Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
 20 25 30
 Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
 35 40 45
 Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
 50 55 60
 Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
 65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 411

gtttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-40

<223> Synthetic construct.

<400> 413

atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcggc ccgcaacact ccgtctcacc ctctgggccc 100
actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctgagccct cgggtggaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctcct gccctcctc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cagctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtccctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttcggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagcccctt gagcagttct 900
taaagaacag ccagacaca aacaaatag agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagtcct gcctgactta ggagtcagag 1050
cccggcaggg gctgaggagg aggagcaggg ggtgctgctt ggaaggtgct 1100
gcaggtcctt gcacgtgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct ggttttgaaa aaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415

Met	Arg	Val	Ser	Gly	Val	Leu	Arg	Leu	Leu	Ala	Leu	Ile	Phe	Ala	1	5	10	15
Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser	20	25	30	
Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr	35	40	45	
Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro	50	55	60	
Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala	65	70	75	
Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met	80	85	90	
Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu	95	100	105	
Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp	110	115	120	
Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu	125	130	135	
Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro	140	145	150	
Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu	155	160	165	
Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val	170	175	180	
Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln	185	190	195	
Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro	200	205	210	
Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	215	220			

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgtctgc tctctctctc tctctctcac tctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcacccttc ctgggacact atgttgttct ccgccctcct gctggagggtg 300
atttggatcc tggtgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccca gctccacctg 600
cactgggggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700
atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatagctt atgaacacat 800
tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850

ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900
cgctacaatg gctcgtcac aactccccct tgctaccaga gtgtgctctg 950
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
ttcagggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatattc 1200
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400
ccttccccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550
gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
tttccttaga tatactgcgg gatctctcct taggataaag agttgctgtt 1650
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala					
				95					100					105					
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
				110					115					120					
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
				125					130					135					
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
				140					145					150					
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
				155					160					165					
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
				170					175					180					
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
				185					190					195					
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
				200					205					210					
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
				215					220					225					
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
				230					235					240					
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
				245					250					255					
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
				260					265					270					
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
				275					280					285					
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
				290					295					300					
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
				305					310					315					
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
				320					325					330					
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
				335															

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 424
 gtaaagtcgc tggccagc 18

 <210> 425
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 425
 cccgatctgc ctgctgta 18

 <210> 426
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 426
 ctgcactgta tggccattat tgtg 24

 <210> 427
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 427
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

 <210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

 <400> 428
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaca 200
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatac 300
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350
 gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
 aaatcttcac gagcctcatc atccattcct tgttcccggg aggcatcctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatac 700
 agcaaataga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
 gaaaatatcc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgctgcct ggatgatatg catattaaaa catatttga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073.

<210> 429
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 429
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg
 1 5 10 15
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
 20 25 30
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
 35 40 45
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
 50 55 60
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
 65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn	
				80					85					90	
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr	
				95					100					105	
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro	
				110					115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly	
				125					130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp	
				140					145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln	
				155					160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp	
				170					175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His	
				185					190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln		
				200					205						

<210> 430
 <211> 1257
 <212> DNA
 <213> Homo Sapien

<400> 430
 ggagagagggc ggcggggtga aaggcgcatc gatgcagcct gcggcggcct 50
 cggagcgcg gggagccaga cgctgaccac gttcctctcc tcggtctcct 100
 ccgcctccag ctccgcgtg cccggcagcc gggagccatg cgaccccagg 150
 gccccgcgc cccccgcag cggctccgcg gcctcctgct gctcctgctg 200
 ctgcagctgc ccgcgcgtc gagcgctct gagatcccca aggggaagca 250
 aaaggcgag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
 aaaattgagg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttcggctaaa atgcagaaat gcatgctgtc 600
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700
aattaatatt catcgcactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900
ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagt 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggctc tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgttaagaat tttttttata tctgttaa ataaaattatt 1250
tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly	1	5	10	15
Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	20	25	30	
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45	
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	95	100	105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135	

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
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